HealthSupport
Queensland
Forensic and Scientific Services

Procedure for Case Management

1 Purpose

The purpose of this procedure is to describe the components of a case record, processes involved in compiling and completing a case record and tracking of case records.

2 Scope

This procedure shall apply to all Forensic DNA Analysis staff that case manage any component of a case record.

3 Definitions

Case record	All information relating to a particular case. This can include all case histories, receipts, communication with clients, examination notes, Analytical data, internal communications, results and reports.
DAD/DADI	The DNA Analysis Database Interface (DADI) is used to maintain the data stored within the DNA Analysis Database (DAD) and to provide results management functions.
GSI	Generic system interface (AUSLAB interface to QPS)
Examining scientist	The scientist/s who has/have examined exhibits for a case.
EXH	Exhibit report (post 8/10/2008)
EXR	Exhibit report (pre 8/10/2008)
Case managing scientist	The scientist(s) that has (or have) been involved in the assessment of results and compilation of the case file in preparation for statement writing or peer review.
In tube	An item that has been sub-sampled by the QPS and submitted to the laboratory in a tube ready for analysis.
Paperless	A type of case that does not involve a traditional paper case file. Work is performed almost entirely in AUSLAB
Paper	A type of case that involves a traditional paper case file.
STRmix™	A statistical program used during case management to interpret certain types of DNA profiles.
DRMU	DNA Results Management Unit – A QPS Unit that transfers the EXR/EXH and LKR results from the Forensic Register to QPRIME. They also perform quality checks on the validity of the information/results received.
Reporting Scientist	The scientist who is responsible for writing a Statement of Witness outlining the results of a case and for presenting evidence in a court of law.
CRISP	Crime Recording Information System for Police (Pre 2008)
QPRIME	Queensland Police Records and Information Management Exchange (Post 2008)
AmpF*ℓ*STR® Profiler Plus®	The amplification kit made by Life Technologies – This is used for low priority cases (Volume crime cases).
AmpF*ℓ*STR® COfiler®	The amplification kit made by Life Technologies – this was used for additional loci in paternity cases. This is no longer used.

PowerPlex® 21 system kit	The amplification kit made by Promega that is currently used for all reference samples and high priority case work samples.
SSLU	Scientific Services Liaison Unit
Modify 8	Code utilised by AUSLAB to perform automated actions with AUSLAB
P+	AmpFℓSTR® Profiler Plus®
PP21	PowerPlex® 21 system kit
ERT	Evidence Recovery team
FRIT	Forensic Reporting and Intelligence Team
VAR	Variant allele
OLA	Off ladder allele
ULP	Unlabelled allele
XOVER	Cross over allele, allele migrates into an adjacent marker bin.
NCIDD	National Criminal Investigation DNA Database
QFLAG	Quality checking procedure to investigate potential staff and elimination database matches
STATSWG	Statistics Working Group
EPG	Electropherogram
GMIDX	GeneMapper ID-X, software used for allele designation after capillary electrophoresis

4 Case file overview

Each case file has a unique case number (Occurrence/QPRIME number, CRISP number or SSF/COR/CA number).
CRISP numbers were used by QPS for cases prior to 2007; the format used is XX/XXXXXX. Occurrence numbers (QPRIME) are generated by QPS and are recorded in AUSLAB with a prefix e.g. QP1400000000. SSF/COR/CA numbers are generated in AUSLAB and usually indicate a coronial matter.

Table 1 - UR prefix summary

UR prefix	Description	Use	Date range
F	F numbers Biol	Historic	1965-2004
QPS	QPS CRISP	Historic	2004 - Mid 2007
QT	QPRIME Temp	Historic	Mid 2007 - 2008
QP	QPRIME	Current cases	Mid 2007 - Present
FBQA	Forensic Biology Q.A	External proficiency	2003 - present
FBOT	FBiology Robotics Validation	Internal Controls	2005 - present
FBE	Forensic Biol Environmental	Environmental monitoring	2005 - present
SSF	SS-Forensic	Generic forensic	2002 - present
COR	QWIC (QLD Magistrates)	Coronial cases	2003 - 2009
CA	Coronial Autopsy	Coronial cases	2009 - present
LKR	Link reports	Link reports	2003 - present

Information relating to a case, such as offence type, is recorded in AUSLAB. See QIS 17116 *Processing DNA Exhibits/Samples in the Forensic Sciences Property Point* and QIS 16004 *AUSLAB Users Manual – DNA Analysis*.

If a case contains items or documentation citing more than one case number, enquiries can be made to the QPS Sample Management Unit (SMU) to establish whether the cases are linked and can be reported together. Details of these checks must be included in the UR notes

All cases registered in AUSLAB will have a CS test panel (case management screen) requested (except for F numbers). The CS is requested on the first laboratory number registered for the case. There should be only one CS test panel for each case. The CS test panel provides general details on the case. The tests displayed on the CS are:

- **Status** (CASEST)–the case status is used to track the workflow in the milestones page. Options for this field are:
  - RECEIVED – case has been received but not allocated.
  - ALLOCATED – case has been allocated
  - AWAITING ADVICE – more information has been requested. Case is on hold until further notice. This status is not tracked in the milestones.
  - STARTED – Examination has commenced
  - SENT TO PEER REVIEW – case has been completed and has been sent for Administrative and/or Technical review.
  - RETURNED FROM PEER REVIEW – case has been returned to Case Scientist for amendments during the review process.
  - REPORT ISSUED – case has been reviewed and statement has been sent. Entered by the reviewer following tech/admin review.
  - ANALYSED - REPORT NOT REQUIRED – case has been reviewed and no statement has been requested. Entered by the reviewer following administrative review.
  - NO TESTING REQUIRED – case has been written off, no work was required or no longer required.
  - REACTIVATED – case has been reopened for more work or statement preparation.
  - ON HOLD SAMPLED AND STORED – Used for low priority cases for samples that have not been sent for processing
- **People involved in the case (Surname, First name, DOB, Class)** – (CSN1-CSN10) names, dates of birth and classes of people involved in the case, e.g. complainants, suspects, defendants, deceased, elimination.
- **Case Scientist** (CSCI) – scientist who has been allocated the case, generally the reporter.
- **Primary Case Scientist** (CSCIP) – allocated case manager or reviewer.
- **Case Type** (CASET) – e.g. Armed Robbery, Assault, Murder, Property, Proficiency Testing, Paternity, Sexual Assault, Coronial/DVI. This is supplied by QPS.
- **Crime Class Code** (CCCODE) – information provided by QPS, subdivisions of the case type categories.
- **Operation** (CASEO) – used to record police operation name if applicable.
- **Investigating Officer** (INVOFF) – Contact officer for the case.
- **Due Date** (FTDC) – date when statements or results are required, used mainly for Coronial/DVI cases or major investigations.
- **Court Date** – date of court proceedings. May be committal or trial. Details are recorded in UR notes.
- **Biol/Police Priority** (FORCAT) – used to assist in case prioritisation.
- **Date Completed** (FBCDAT) – date case review is completed.
- **Exhibits** (EXRTR) – indicates status of exhibits.

4.1 When is a case file required?

Since the 1st of September 2009, low priority Volume Crime cases have been treated as 'paperless' and therefore do not have case files. In April 2010, paperless case management and review was expanded to also include all cases of both high and low priority (Volume and Major Crime) and some Sexual Assault cases (Yellow Team cases) except for cases

involving excessive numbers of crime scene/reference samples or complex profiles. In April 2015 all cases are initially managed as paperless cases.

Case files are generally created

- At the time of case management (for complex cases) or
- When a statement is requested or
- When a case manager/reporter deems it necessary for efficient case management.

A case that has been initially managed paperlessly may be converted to a paper file if further exhibits are received at a later date. Case and examination notes are stored in 'Paperless' folders stored in Evidence Recovery, Reporting and Admin areas.

If a case has been converted from paperless to paper, it is not necessary to annotate all of the epgs with the interpretations unless a statement has been requested. The reporter of the statement will update the epgs with interpretations as they are documented in AUSLAB.

4.2 How to create a case file

Additional information is provided in QIS 24126 *DNA Analysis Unit Administrative Officer Case Management*. It is advisable for efficiency purposes that casefiles are created by the Forensic DNA Analysis Administration Team.
To request a casefile to be created, email FSS_DNA_Analysis_Admin@health.qld.gov.au with instructions. Alternatively, instructions are given below:

1. Check AUSLAB to see if a case file already exists. If a file does exist, a new one does not need to be prepared and the file should be located.
2. If a file does not exist and it has been determined that one is required, it will need to be prepared.
3. Place a barcode for the first received receipt (if multiple receipts are registered) on the case file folder in the box in the top right hand corner labelled 'case barcode'. This first receipt barcode should also be the barcode that the CS screen is registered under in AUSLAB. See Appendix 1 for details on the CS screen.
4. Write the case number at the top of the folder in the 'Case Number' field.
5. If applicable, write the initials of the reporting scientist in the 'Reporting Scientist' field. If no statement is to be issued, this field should have 'N/A' entered in it.
6. Write the complainant's and suspect's/defendant's names (if known) on the lines next to the 'NAMES' fields (one name per line). Surnames should be written in capitals and given names in lower case. Write '(Comp/Def't)' or '(Sus)' after each name as appropriate. If the complainant is a company, the company name can be written on the case file, but for reporting purposes the complainant in these cases is 'Regina'.
7. Turn the folder to the side and fill out the details along the edge as indicated: case number; case type - found on the CS screen for the case in AUSLAB, e.g. assault (N/S); names - divide the line in half with a diagonal line and write the surname of the complainant on the left side and the surname of the suspect(s)/defendant(s) (one on top of the other if necessary) on the right side.
8. Place the receipt barcode on the Case File Particulars page (QIS 17038) in the box in the top left hand side of the page labelled 'Case File Barcode'. If no barcodes are available, print a new barcode from AUSLAB.
9. On the Case File Particulars page write the case number in the 'Case #' field.
10. Place the Case File Particulars page and receipt page(s) (scanned signed copies of the receipt) inside the case file and track the file in AUSLAB to the appropriate storage location. Since 26th September 2011, the QP127 (if provided) will be scanned into AUSLAB by Property Point staff and the original handed back to the QPS Officer with the exception of SAIKs where the QP127 will be scanned into

AUSLAB and attached to the GMO notes, tracked and transferred to Forensic DNA Analysis.

4.3 Additional Elements of a case file

Upon completion, a case file may also contain:

1. Examination notes
2. Diagrams, photographs and/or photocopies
3. Statistical calculations
4. Copies of results (Genotyper or GeneMapper ID-X printouts)
5. Interpretations of results
6. Copy of statement or intelligence report
7. Records of any internal or external communication relating to the case, e.g. UR notes or emails.
8. STRmix™ output files

4.4 Handwritten results and corrections within a case file

As is required by NATA ISO 17025 - as case notes etc. are subject to subpoenas; no pencil is to be used in the case file (unless used in diagrams or pictorial representations).

Any calculations, interpretations or changes to notes or results must be initialled and dated by the person performing the action.

4.5 Case file storage and movement

Case files are required to be kept indefinitely as per accreditation requirements.

1. No exhibits are to be stored in the case file. This includes external proficiency samples. Original QPS property tags or reference sample envelopes are also NOT to be stored in the case file.
2. Case file movement is to be recorded in AUSLAB.
3. Active case files are stored with the case analyst or in a designated storage location for the work area.
4. Upon completion, scientists should transfer cases to either FBCFF1 (Case File Finish) or FBPR1. Administration assistance slips are available to attach to the front of the case file to direct the storage of the file or to outline any further administrative tasks that need to be performed prior to storage.
5. FBCFF1 is the location from which administrative staff will track case files (sequentially) into the compactus or another designated storage location. No further administrative tasks will be carried out on these cases.
6. FBPR1 is the location which administrative staff will collect cases from in order to perform further administrative tasks such as page numbering and administrative reviews (left hand side only).

5 Workflows

5.1 Priorities

Table 2 details the DNA priorities that are used in Forensic DNA Analysis. These are not to be confused with case priorities. Case priorities are received from the QPS via the Forensic Register interface.

Table 2 - DNA Priorities in Forensic DNA Analysis

Priority	Description	CW Use	Ref Use
1~SS	Urgent	Urgent	Priority/investigation
2~SS	High Pri	Major crime	High priority
3~SS	Med Pri	Volume	Normal
4~SS	Low Pri	No longer used	N/A
5~SS	Very low	No longer used	N/A
6~SS	Cease	Cease work	Cease work

Urgent (5 day TAT) cases are specifically allocated to a case scientist and/or reporting scientist as they arrive into the department. The Management Team will be notified of the arrival of an urgent case by email and appropriate UR notes will be entered. A supervising scientist will allocate to an appropriate case manager. This does not mean that the case managing scientist will necessarily become the reporting scientist should a statement be required.

Priority 1 samples will be list inserted to the GREECM so they can be monitored by the Intelligence Team. The Supervising scientist or the case manager will list insert the case to their communication list. They must be managed as soon as results become available and reviewed as soon as results are interpreted. To ensure there is no delay in QPS being informed of 5 day TAT results as soon as they are available, a workflow has been created for samples that are expected to be completed on a Friday. See QIS 17119 *Procedure for the Release of Results*. Reworks on priority 1 samples are to be ordered and case managed by the original allocated scientist.

Priorities 4 & 5 are no longer used; if a sample has one of these priorities and needs to be case managed the priority must be changed to 3.

5.2 PowerPlex®21 system kit vs AmpFℓSTR® Profiler Plus® case management

Cases that have been started in one STR system will generally be completed in that system. The exception to this single system testing is reactivation and receipt of further exhibits for a high priority case that has been tested with AmpFℓSTR® Profiler Plus® (P+). These samples can be processed in PowerPlex®21 system kit (PP21) if the previous results were all reported as 'No DNA detected'. Approval from a Team Leader or the Managing Scientist is required in this scenario. Other exceptions include specific requests from QPS Insp for DNA Results Management Section/ Senior Sergeant delegate to a Forensic DNA Analysis Team Leader.

All major crime cases that have been allocated a case priority of 1 or 2 are processed in PP21 with a DNA priority of 1 or 2. All other cases are processed in P+ (Volume priority 3).

New evidence samples received for a case which has been profiled using P+ will be profiled using PP21. Only the 9 common loci between kits will be used for comparison purposes. For cases where a statement is required, a paragraph explaining the comparison of P+ casework samples and PP21 reference samples must be entered in the preambles section. See also QIS 17119.

5.3 STRmix versions

Any cases with a priority 1 or 2 received from Jan 1 2015 are processed with STRmix™ version 2.0.6 Refer to QIS 31523 *Use of STRmix™ Software*. All likelihood ratios (LRs) are

generated using STRmix™ v2.0.6 regardless of the version of the deconvolution. See Table 3 below.

Table 3 – STRmix version use

Date case received	Decon	LR (at time of receival)	LR (New comparison)
19 Dec 2012 – 30 June 2014	v1.05	v1.05	v2.0.6
1 July 2014 – Jan 2015	v2.0.1	v2.0.1	v2.0.6
30 Jan 2015 – present	v2.0.6	v2.0.6	v2.0.6

5.4 Case management workflows

See Appendix 1 for a high level overview of case management lists/batches used.

Allocation of cases to a particular scientist usually only happens if a statement is required, the case is large or has been assigned an Operation by QPS. These cases will otherwise be routinely case managed by the Reporting and Intelligence teams. However, to reduce the amount of double handling by case managers, individual samples initially case managed by a particular person will be completed by the same person. This includes reworking and STRmix deconvolutions.

Unallocated paper case file may be stored in the FRITCM filing cabinets stored in the far end of the reporting area in Block 3.

Internal controls, external and internal proficiency, internal and external environmental monitoring samples case managed by the Analytical, Evidence recovery and Quality teams. The presence of these teams in the BTEAMS field triggers the Modify 8 equation to list insert to the 1AS (Analytical), ERT (Evidence recovery) or BQUAL (Quality) lists.

At the time the results of the DNA profiling are imported into AUSLAB; pre configured autovalidation rules (contained within the results import autovalidation mask) add a test (BID1, BID2 or BID3) determined by the presence of a core comment. The Modify 8 equation is triggered to list insert these samples onto workflow lists if certain requirements are met.

1. When the Sample Status (**XPRES**) or DNA Profile Result (**9PLEXS**) is "PDF ready" the system checks to see if the sample is ready for case management. This is defined in the system as incomplete or complete sample statuses and the plate reading comment matching the BID test ordered.
    i. If the sample statuses are incomplete the Modify 8 equation list inserts the sample to the appropriate hold list
    ii. If the sample statuses are complete the Modify 8 equation lists inserts the sample to the appropriate case management list.
2. Following case management of PP21 samples, the samples can be added to the STRMX deconvolution list if HP2 assistance is required by changing the Sample Status to 'STRmix decon'. This triggers the Modify 8 equation to list insert to the sample to the STRMIX list and list removes from the current case management list.
    i. The comments field of the XPLEX page should have clear instructions for the STRmix operator, as opposed to an interpretation note for case managers.
    ii. Suggested instruction format for STRmix: 'STRmix: v2, 3p/LR'. Suggested format for interpretation: 'CM: 3p drop D21 tri'. If STRmix and interpretation notes are wanting to be added to the comments field together, the suggested format is: 'STRmix: v2, 3p/LR | CM: 3p drop D21 tri'.

3. On completion of this task the HP2 will change the Sample status of the sample to 'STRmix complete'. This triggers the Modify 8 equation to auto list insert to the STRMXCM (STRmix CM) list and list remove from the STRMX list.
4. Samples are manually list inserted to the appropriate review list, adding the Sample status (**XPRES**) of 'For Review' triggers auto-list removal from the current list.

Table 4 - Criteria to direct samples to appropriate lists

Test	GMIDX CORE COMMENT	BID TESTCODE	ON HOLD LIST	CM LIST
XPLEX	NSD	BID1	SSHOLD	SSCM
XPLEX	SS	BID1	SSHOLD	SSCM
XPLEX	MIX	BID2	MIXHOLD	MIXCM
XPLEX	COMPLEX	BID3	COMPHOLD	COMPCM
XPLEX	(BLANK/no Core Comment)	(NONE)	(NONE)	BLCM
9PLEX	NSD	BID1	(NONE)	VOLLOW
9PLEX	SS	BID1	(NONE)	VOLLOW
9PLEX	MIX	BID2	(NONE)	VOLLOW
9PLEX	COMPLEX	BID3	(NONE)	VOLLOW
9PLEX	(BLANK/no Core Comment)	(NONE)	(NONE)	BLCM

The hold lists are SSHOLD (SS On Hold), MIXHOLD (MIX On Hold), COMPHOLD (Complex On Hold) and VOLHOLD (Volume On Hold).

The case management lists are – SSCM (Single source case management), MIXCM (Mixture Case Management), COMPCM (Complex Case Management) and VOLLOW (Volume Low priority).

A further list BLCM (No team Case management) is utilised for samples that do not contain a core plate reading comment. This is managed by the FRIT Team Leader.

The 'Hold' and 'Case management' lists are sorted by the Case Manager field, then the request date. See Figure 1 below.

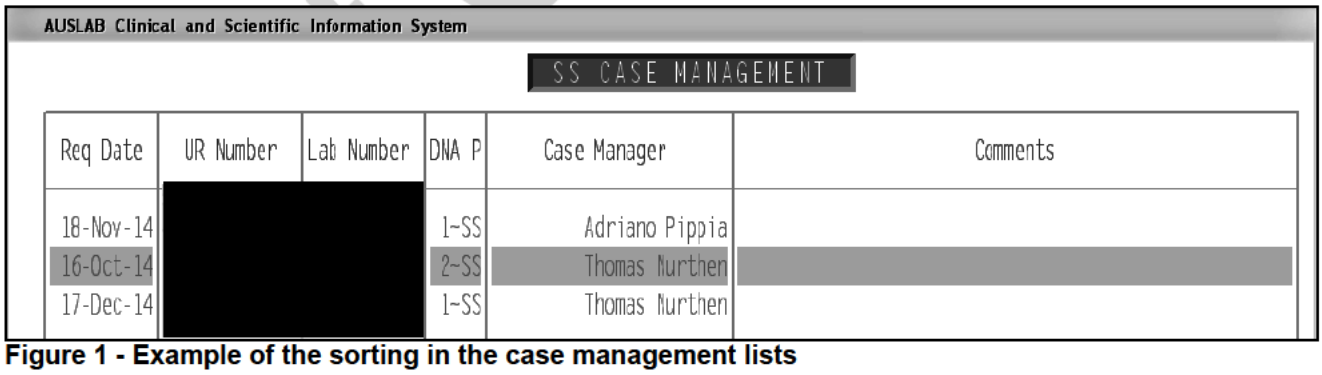

Figure 1 - Example of the sorting in the case management lists

Review of results is managed through the following AUSLAB worklists: SSREV (single source review), SSUPREV (Single Source Upload Rev), MIXREV (Mixture Review), MIXUPREV (Mixture Upload Review), COMPREV (Complex Review), VCREV (Vol Review) and VCMIX (Volume Paperless Mixtures) or for paper case files, MIXACT or the reviewer's storage location.

Various tools may be employed to assist in meeting timeframes and to cover absence such as scheduling Outlook appointments or tasks.

Rework tests ordered on samples trigger the Modify 8 Equation to remove the sample from the current list.

6 Case management

The purpose of case management is to collate and report any DNA results that have been obtained and to prepare the case file for a statement (if required) or for peer review. To achieve this, the case managing scientist may be required to:

1. Assess DNA results to determine whether reworking is required to improve or confirm results.
2. Assess reworked and initial results to determine which is the best profile (for P+ cases only).
3. Enter final EXR/EXH results into AUSLAB.
4. Compile case file and finalise AUSLAB pages.

The steps for case management are listed below and a checklist provided in Appendix 2.

6.1 Check quality

Samples should not be progressed or reported until the various quality checks that are in place have been completed. These checks are designed to identify potential issues with samples before they are reported to the QPS.

6.1.1 Batch statuses

Check that the statuses of the processing batches are fully completed (XPLEX samples will have up to five test panels that list batch statuses (PLEXB,PLEXC,PLEXD,MCONC and NSPNC panels - See Figure 2). Please note that 9PLEX batches only have a final batch ID for each rework and no status fields. 9PLEX samples that require further consideration will have a 'See batch audit' specimen note.

Samples under investigation will have a batch status of 'Investigation'. These samples will not have an end date and will populate the appropriate 'hold' list until the investigation is complete.

Absent batch statuses may indicate a batch has not undergone final quality checks. Do not case manage samples unless there is a batch status or you have checked the status of the batch from the batch audit itself. If this is the case, then add a specimen note to indicate what has been checked and why.

If the batch has been passed without any issues the status will be 'Pass'. This status does not require any checking of the batch audit.

It is optional for the case manager to check the batch audit if the batch status is 'EXTN < 3pks'.

If there has been an issue noted during processing of a sample, the Analytical staff member/delegate will enter a status of 'See batch'. The case manager **MUST** check the batch audit and add a specimen note to indicate what the issue is and that it has been assessed and they have deemed the sample OK to report.

Test	Started on	Batch Id	Completed on	Batch Status	Processing Comment
XPLEX					
	17-Jul-14	[redacted]	17-Jul-14	Passed	
	17-Jul-14		17-Jul-14	Passed	
	17-Jul-14		17-Jul-14	Passed	
	17-Jul-14		17-Jul-14	Passed	
	17-Jul-14		17-Jul-14	Passed	

Figure 2 - XPLEX request (PLEXB page)

6.1.2 UR notes

Check UR notes for relevant information. UR notes are the repository for information that relates to a whole case. Information such as allocation to an individual case manager/reporter, SAIK strategies, court timeframes, communication with DRMU etc are recorded in the UR notes.

6.1.3 Specimen notes

Check for relevant information in the specimen notes. Specimen notes are used when information is specific to that laboratory number. Specimen notes are used for communication regarding processing. .e.g. that an issue raised in a batch audit has been assessed by the case manager.

6.1.4 Digital images

Check the digital images attached to the record in AUSLAB. These may be photo(s) of the exhibit(s), exhibit packaging or labelling.
To check the digital images, access the digital imaging component of AUSLAB

- From the sample barcode press [**CTRL + INSERT**]
- A list of all of the images for that barcode will appear
- Select an entry and press [**Enter**]

If the samples are 'In tube', the details on the envelope should match those registered in AUSLAB. If they do not and no action has already been taken refer to Section 4 of QIS 26071 *Examination of In-tube samples*.

For whole items, check the image and barcodes in the image match descriptions in AUSLAB.

For additional information on digital imaging refer to QIS 20080 *Digital Imaging in DNA Analysis*.

6.2 Check case information

Case information may be relevant to only particular samples or the whole case. This information may be used to guide the case manager's choice of processing and reporting.

6.2.1 Check for reference samples associated to the case

The presence or absence of reference samples may affect the workflow path a sample takes. If reference samples have been received for a case, these will be compared against

representative single source DNA profiles, all interpretable mixed DNA profiles to generate a LR (XPLEX only) or to attribute contributions e.g. major, minor DNA profiles (9PLEX) and reported back to QPS via EXH/EXRs.

1. From any test panel in the case, press **[SF9]**
2. Page through the list and look for the specimen type FTA Evidence or FTA Specimen -Elimination (Intel purposes).

Alternatively the association of a reference sample to a case is documented by SSLU/Laboratory staff in the UR notes.

FTA specimens- Elimination (Intel Purposes) are associated to the case file but are not used in statements. The result of the comparison is reported back via an EXH the same as Suspect checks.
FTA specimens may **only** be used for comparisons if the QPS have requested a suspect check.

6.2.2 Check for case allocation

It is necessary to check if a case has been allocated to a particular case manager or reporter before case managing a sample. Check the CSCI field on the CS test panel or the UR notes to see if a case has been allocated.

6.2.3 Check for paper file/case notes.

Check the AUSLAB storage locations to see if a paper file has been created.

1. Press **[SF9]**
2. Press **[SF5] Specimen Search**, check for specimen type 'Case File' and take note of the storage location and description

This method can result in known display issues if the rack descriptions are too long.

Another method is listed below.

1. Press **[SF9]**
2. Select the entry with the CS request and press **[Enter]**
3. Press **[SF8]** Audit
4. Press **[SF8] Storage Audit**
5. Take note of the storage rack mnemonic.

If you are unsure whether the mnemonic refers to a paperless location or an actual case file check in the AUSLAB storage

- **Main Menu**
- Select **2. Sample Processing**
- Select **6. Sample Storage**
- Enter the mnemonic in the Rack Name field and press **[Enter]**

The screen will update and the Rack name and Location will be displayed.
If a paper case file exists; results and interpretations must be printed and filed in the case file. This includes the epg and STRmix deconvolutions. Reviews of the results in a paper case file are managed through the MIXACT or individual intray location as per Section 8 below.

6.2.4 Check ownership of item

Ownership of an item may be required before interpretation of a DNA profile or an exhibit is sampled. The ***ELF*** (***Item Ownership***) AUSLAB list is for requesting ownership details of items. This information can be requested by the Evidence Recovery team (ERT) before or

at the time of registration/sampling or by a case manager. Add the details required to the AUSLAB specimen notes and list insert to the ELF list.

SSLU give the QPS three days to respond to the request before they contact them for a follow up.

6.2.5 Check case status

The case status in AUSLAB is sent back to the QPS via the GSI interface. As the status is changed the details are recorded in the FBMILE (Milestone page). The order in which the case status must be changed to update the Milestone page in AUSLAB correctly is *Received→Allocated→Started→Sent to Peer.*

Information may be received that indicates that a case is no longer required. This may be in the form of an email from the QPS,a UR note, an 'N' appearing in the Forensic Relationship field for a case/sample in AUSLAB, or insertion on the FBNLR work list by SSLU. Staff are rostered to FBNLR list for a week at a time.
For cases dated prior to September 2009: for items no longer required, SSLU will add NWQPS into the EXH, case manager will finalise case.

For cases dated September 2009 onwards: SSLU will add the relevant samples to FBNLR list, case manager will add appropriate EXH (NWQPS or NWQPSR) and will finalise case.

If notification is received that work is no longer required, yet the sample is at profile interpretation review stage, there is no need to complete the interpretation review. The EXH line 'NWQPSR' (No further work required as per QPS – results available) should be used to inform QPS that there are results, but no further work has been conducted for now based on advice. Any associated AUSLAB pages (eg. COMIX) can be removed from AUSLAB, or completed in such a way that the allele designations do not inform any other case management actions eg. NCIDD loading.

If the EXH 'NWQPSR' is reported back for a sample, and QPS decide that results are required, SMU will advise SSLU via email. This will then be communicated by SSLU via the CSRC AUSLAB work list so that case can be reactivated and the relevant sample(s) reported. The priority will be consistent with the case type.

If work is to be re-started on a sample at a later date due to a priority upgrade or advice from QPS, order a re-work test code as normal and change the priority as appropriate. If the sample had not been extracted prior to the CWORK being ordered, a second barcode is required in the same way that re-extracts are ordered. An appropriate EXH line should also be entered for samples that have been re-started, for example, 'Testing restarted on advice from QPS' (refer to QIS 23008 *Explanations of EXR/EXH Results* for further detail).

6.2.5.1 Finalising samples no longer required

1. Open the ***FBNLR*** list in AUSLAB.
2. Check the ***Forensic relationship*** field and UR notes/scanned emails(some sample may still require testing)
3. Check the testing status of the samples not required.
   a. If the samples have not been allocated to amplification, capillary electrophoresis or GeneMapper batches, order a cease work (**CWORK**) rework test.
      i. Change the DNA priority of the sample to '6'
      ii. Complete the fields on the cease work screen and press [***F6***] ***Validate***
      iii. Enter the final EXH result 'NWQPS' – into the next available EXH line

b. If the samples have been allocated to an amplification, capillary electrophoresis or GeneMapper batch
   i. Enter the final EXH result 'NWQPSR' – into the next available EXH line

4. Enter 'Rev' and Press **[F6]** ***Validate***
5. Press **[F6]** ***Validate*** on the FBEXAM screen if not already validated.
6. If the ***Completed*** date (***9PLCD*** for the 9PLEX panel or ***XPCD*** for the XPLEX panel) is empty, add the current date (t)
7. Add your name to the case manager field (***XPCM*** for XPLEX, ***CSCI*** for 9PLEX)
8. Enter 'N' in the **CM NCIDD** field
9. Enter 'N' in the **Rev NCIDD** field
10. Enter 'N/A' in the ***Review*** field (***XPRV*** for XPLEX or ***9PLREV*** for 9PLEX)
11. Enter 'Finished' (for 9PLEX): or 'Completed' (for XPLEX) into the ***Sample Status***
12. Press **[F6]** ***Validate*** for each of the batch status pages if they are not already validated.
13. Remove the sample from the appropriate 'on hold' or case management list.
14. Remove from the FBNLR list
15. If the whole case is not required
    a. Change the **Status** (CASET) to 'NOTRQ'
    b. Complete the **Exhibits** (EXRTR) field. Most of the time this will be 'DESTR', 'RTORSR' or 'N/A' (e.g. paternity cases)
    c. Add the current date to the **Date Completed** (FBCDAT) field
    d. Delete the Administrative review test panel FBAR
    e. Validate all test panels
16. If a paper case file exists
    a. Add a comment to the case file particulars – 'No longer required'
    b. Track the case file to FBPR1

If

6.3 Assess results

All samples have alleles designated as per QIS 17137 *Procedure for STR fragment analysis using GeneMapper ID-X software* or QIS 31389 *STR fragment analysis of PowerPlex® 21 profiles using GeneMapper® ID-X software*.

When results become available for a sample, an assessment needs to be made as to whether reworks are required or whether sufficient information has already been obtained. This can be performed as each result becomes available. Not all results need to be available at the same time for these assessments to take place.

Samples that have been processed in Profiler Plus have their epgs saved to AUSLAB via digital imaging.

To aid in the assessment of results, several macros have been created. The PDF finder macro locates the epgs (both zooms and standard) for a particular laboratory number or a whole case.

1. Open the macro (I:\Macros\PDF Finder.xls)
2. Click the Find all .pdf files button
3. Enter the required laboratory number or case number
4. Select the years to search by ticking the year required
5. Press the Search button or 'Enter' key
6. A list of .pdf files will be displayed
7. Select the .pdf required and double click or press the open .pdf button.

The Stutter check macro is a tool used to check the stutter and potential pull up for a whole plate or a single sample. The macro uses the allele sizes, allele peak heights, and validated stutter thresholds. This macro is only used for the assessment of PowerPlex®21 samples as stutter is left on and modelled by STRmix™.

1. Open the macro (I:\Macros\Macros to update\Stutter Check.xls)
2. Click the Check for Stutters (1 sample) button
3. Enter the laboratory number in the Sample ID field
4. Enter the GeneMapper plate ID in the Plate field
5. Press Ok button.

6.3.1 Assess the number of contributors to the DNA profile

The number of contributors to a DNA profile is required to perform interpretation. Counting the number of alleles at each locus is the first step in assessing the number of contributors. However, counting called peaks alone may not be suitable in determining the number of contributors due to the presence of PCR artefacts such as stutter. Allelic imbalance (AI) also known as heterozygote balance (Hb) can also be used as an indication of the number of contributors. Forensic DNA Analysis does not have a threshold for AI for casework DNA profiles because STRmix is designed to model the heterozygote balance as a continuous system. Although internal validation studies indicate that the calculated AI threshold varies depending on the DNA input, the values detailed in the study can be used as a guide.

The document '*Assessment of the Number of Contributors for Mixed PowerPlex® 21 DNA Profiles within Forensic DNA Analysis_version 2*' is used as a guideline for determining the number contributors within a PowerPlex 21 sample.

The validated stutter thresholds (as published in QIS 31389 for PowerPlex 21 samples and QIS 17137 for Profiler Plus samples) are used as a guide to aid in the determination of contributors to a DNA profile.

Additional information (for Profiler Plus samples only) is detailed in the document '*A guideline for the assessment of complex DNA profiles*'.

6.3.2 Assess the overall quality of the DNA profile

The quality of the DNA profile in conjunction with the number of contributors will determine if a DNA profile is suitable for interpretation.
The following factors should be considered

1. Whether a reasonable assumption of the number of contributors can be made.
2. The degradation slope (the tendency for higher molecular weight loci to have lower peak heights compared with smaller molecular weight loci).
3. The total amount of DNA input used in the amplification.
4. Adverse events affecting the sample.

6.3.3 Check VAR/OLA/ULP/XOVER calculations

If a variant and/or off ladder allele or stutter has been observed on a GeneMapper ID-X (GMIDX) profile it is not necessary to re-amplify to confirm its presence.

For mixed DNA profiles with variant and/or off ladder alleles, the repeat of these samples is at the case manager/reporter's discretion. Things to consider include whether the profile with variant and/or off ladder alleles has already had this questioned allele confirmed, matches a deconvoluted contribution, or if the sample description suggests the mixed DNA

profile could be conditioned on the reference DNA profile (with variant and/or off ladder alleles).

The case manager must independently perform the calculation for allele designation including if the calculated allele falls in the stutter position. Refer to QIS 17137 or QIS 31389 for details. The case manager must also agree with the calculation performed by the plate reading scientist (enter a specimen note stating this). In the absence of an extract, a re-run is acceptable.

Variant/OLA/ULP/crossover calculations do not require checking if the DNA profile has been assessed as unsuitable for interpretation.

6.3.4 NAD samples

If a sample is flagged as No Analysed Data (NAD) at CE quality checking stage, the sample will be re-prepared by Analytical staff. To confirm the DNA profile is correct and has not been taken from a different well the sample needs to be re-amplified to confirm.

6.3.5 Edit DNA profiles

As interpretation of PP21 samples uses a continuous method of interpretation (STRmix™) rather than a binary method of interpretation, the homozygote and stutter thresholds are used only to guide the scientist in assessing the number of contributors to a DNA profile.

At the plate reading stage of PP21 casework plates, readers do not apply any homozygous threshold. Similarly, putative stutter peaks are not removed from the DNA profile as this information is required by the STRmix™ program for modelling. Following plate reading, PowerPlex®21 casework plates are processed by a macro (QIS 26045 *GeneMapper ID-X File Conversion*) to call a single peak at a locus (for example'15', rather than '15,-' or '15,NR', regardless of peak height.) for AUSLAB upload , to check against the staff database, and create a STRmix upload file.

For single source samples that require NCIDD upload , After processing in STRmix™, the case manager will then change the allele designation in AUSLAB (via the **[SF7]** ***Results History***) to either '15,15' or '15,NR' (based on the STRmix™ deconvolution). The amended profile will then need to be re-saved or edited on the XPLEX page.

Peaks that have been assessed by the case manager to be removed or re-added are list inserted to the 1JMM list for a profile edit. In the specimen notes add the locus name, locus designation to be removed or added, the test name, GeneMapper IDX batch ID and reason. The person editing the DNA profiles from the 1JMM list will liaise with the case manager if the edit is disputed.

The procedure for editing a DNA profile is outlined in section 8.8 Changing Completed GeneMapper Profiles within the QIS 31389. This is a weekly rostered task performed by a competent plate reader.

The DNA profile should be amended in AUSLAB (via the **[SF7]** ***Results History***) by the case manager and if there is a paper case file, reprint the corrected epg.

6.3.6 Rework DNA extract if necessary.

QPS in conjunction with Forensic DNA Analysis have decided that if reworking is required, that additional testing will only be conducted on Major Crime samples and selected Volume Crime samples (high priority cases - DNA priorities 1 & 2) via any means available.

For PP21:
Internal validation studies have shown that samples with low template DNA (~132 pg) that are amplified with PP21 may exhibit significant stochastic effects such as large allelic imbalance and allele drop-out. These effects can complicate the interpretation of both single source and mixed DNA profiles. Reworking may improve the quality of the DNA profile.

For P+:
Low priority Volume Crime (DNA priority 3) cases are only to be reworked via re-amplification, re-running (previously known as re-Genescanning) or re-reading in GMIDX until 12 alleles are obtained (National Criminal Investigation DNA Database-NCIDD uploading threshold). No NucleoSpin cleanups or Microcon concentrations are to be ordered on low priority samples. Other valid reasons for reworking these samples include investigations of adverse events or other quality issues are suspected.

If allelic imbalance occurs (<70% in a Genotyper profile or <50% in a GMIDX profile), the alleles can be reported as single source if the case managing scientist is confident that both alleles at the locus are paired from a single contributor. The profile should be examined carefully for evidence of a mixture; if there is no evidence of a mixture both alleles can be reported. The case managing scientist wanting to accept the alleles as true should record this on the epg. For paperless cases this is recorded in the specimen notes for the sample. By validating the 9PLEX page for such a sample, the reviewing scientist is agreeing that they approve of this interpretation.

If a partial profile or NSD profile is obtained for a sample, an assessment should be made as to whether reworking that sample will be beneficial or if there are other profiles within the case that satisfy reporting requirements.

Rework strategies:
If it is determined that a better profile is required, the following should be considered when determining the best rework strategy:

1. **The type of sample**
   e.g. blood versus cells. Due to the generally high number of nucleated white cells in whole blood, a DNA profile is usually obtained from such samples. On the other hand, shed skin cells contain few or no nuclei and therefore it is more difficult to obtain a profile of DNA that has been deposited on an item through casual contact.

2. **The quantitation value**
   The quantitation value is displayed in the 'FBQUAN' or 'QUANT' field in AUSLAB. The quantitation value is an estimate and should be assessed in conjunction with other factors. Sample workflows based on the quantitation value are listed below:
   See also Appendix 3 – Quantitation

   1. P+ samples with an undetermined quantitation value will not be further processed and will be reported in their associated EXH as 'No DNA detected', regardless of priority.
   2. P+ samples with any detectable quantitation value will be amplified.
   3. P+ samples in cases that were previously High Priority (P2) that require a microcon rework (MICFCW), need to have instructions added to the Processing comments for the type of microcon eg. Mic to full, mic to half, mic to 30uL.

4. PP21 samples with a quantitation value <0.001 ng/µL will not be further processed and will be reported in their associated EXH as 'No DNA detected', regardless of priority.
5. PP21 QPS environmental samples with a quantitation value of >0.001 ng/µL but <0.0088 ng/µL as per QPS –Forensic DNA Analysis agreement will not be routinely amplified or sent for Microcon processing. This result will be communicated using the 'DNA insufficient for further processing' EXH line.
6. PP21 samples with an initial quantitation value between 0.001 ng/µL and 0.0088 ng/µL will automatically be sent for a Microcon to 35 µL and be re-quantitated then amplified.
7. PP21 samples with an initial quantitation value of > 0.0088 ng/µL are amplified.

A partial or NSD profile from a sample with a high quantitation value may indicate inhibition. It should be noted that while quantitation values can be used as an indicator for the presence of inhibitory compounds in an extracted sample, lack of inhibition in a quantitation amplification (as indicated by the IPCCT and possibly the CT as well) does not necessarily mean there will be no inhibition in an STR amplification. This is because different primers, target DNA and amplification conditions are used in each reaction and this could result in inhibition to one reaction and not the other. Also, 2 µL of extracted sample is added to a quantitation amplification, whereas in an STR amplification the sample may be diluted before being added (which would decrease the concentration of any inhibitory substances in the amplification reaction), or up to 20 µL may be added to the reaction for a P+ sample, 15 µL for a PP21 full volume amplification (which would change the relative concentration of inhibitory substances in the amplification reaction). Further information on DNA quantification is found in QIS 33407 *Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit*.

There may be additional quantitation information available for a sample (depending on whether it was processed pre/post AUSLAB batch functionality)

3. The number of alleles obtained

A full DNA profile is the aim of any DNA amplification but a partial DNA profile does not necessarily need to be reworked.

The minimum number of alleles required to upload to NCIDD is 12 alleles. Samples below this stringency, but above 6 alleles, may be loaded to NCIDD under special circumstances and searched against the database (refer to QIS 23890 *Uploading and Actioning Samples on NCIDD*.

If an assumption of a single contributor has been determined, Partial DNA profiles do not have to be reworked to obtain a full DNA profile.

4. Examination notes

Certain substances are known to be inhibitory to the PCR process. This includes a variety of commonly encountered substances, such as dyes used in clothing (particularly denim dyes) and some biological material (in particular, the haem in blood). Semen samples have also been observed to return an NSD profile after initial extraction with no indication of inhibition. Performing a NucleoSpin clean up may result in improved or full profiles for these samples.

5. **Offence Details (if available)**
   The information from the QP127, item packaging or from case conferences may assist in determining the evidential value of a particular item. If the case has a paper file, it will already have been printed and added to the file, if it hasn't or for paperless cases the QP127 will have been scanned into AUSLAB usually on the case barcode.

6. **Results already obtained**
   If multiple samples have been submitted for an item and one or more full profiles or mixtures have already been obtained there may be no need to continue reworking other samples from that same item. A partial 'matching' profile is often sufficient if other better profiles already exist for the same item. This must be considered carefully and in the context of the case. If it is a possibility that there may be a different profile present, such as in the case of multiple offenders, then reworks should be considered.

AmpFℓSTR® COfiler®
Prior to samples routinely being processed using PP21, additional work using the AmpFℓSTR® COfiler® (COfiler) kit could be ordered if required. Samples processed using the P+ kit could be amplified with the COfiler kit in order to amplify an additional 4 loci.

Reworks on AUSLAB batch functionality samples
When requesting reworks ensure that the case scientist field (**XPCM**) is completed; this will reduce double handling as the same case manager will take ownership of that particular sample.

All reworks for current samples are carried out through the **[SF7]** ***Results History*** screen of the sample as per QIS 24469 *Batch Functionality in AUSLAB*.
Specific tests codes are available for each rework. Refer to Table 5 below and QIS 24486 *Explanations of Analytical Test Codes and Batch Types* for the reworks available in AUSLAB and the test codes to be used.

Table { SEQ Table * ARABIC } - Case work test panel and rework tests

Description	XPLEX Panel	Processing Comment	9PLEX Panel	Processing Comment
Primary test panel	XPLEX	XPC1	9PLEX	9PLEXP
Re-Amplification	XAMP1	XPC2	AMP1CW	N/A
Re-Amplification	XAMP2	XPC3	AMP2CW	N/A
Re-Amplification	XAMP3	XPC4	AMP3CW	N/A
Re-Quantification	XREQC	XPC7	REQC	N/A
Microcon procedure	MCONC1	XPC8	MICFCW	MICFCP
Microcon procedure	MCONC2	XPC9	MICCW2	MICF2P
Re-Run	XRRC	XPC5	RRCW	RRCWP
Re-Run	XRRC2	XPC6	RRCW2	RRCW2P
NucleoSpin clean up	NSPNC1	XPC10	NCLCW	NCLCWP
NucleoSpin clean up	NSPNC2	XPC11	NCLCW2	NCLC2P
Re-Read	N/A	N/A	GMCW	

The total PCR volume used for a PP21 amplification is 25 µL and P+ amplification is 50 µL and the corresponding total allowable sample volume (SV1) is 15 µL and 20 µL respectively.

SV1 and TV1 must add up to 15 µL (for XPLEX) and 20 µL (for 9PLEX).

SV2 and TV2 are used when a dilution is required.SV2 and TV2 combined cannot exceed 20 µL. If a dilution is not required these must be filled in as '0'. To enter the volumes required for a dilution see QIS 24012 *Miscellaneous Analytical Section Tasks*.

The MultiPROBE® II PLUS HT EX Forensic Workstations are unable to pipette volumes of less than 1 µL, concentrated samples should be diluted so that the minimum volume is 1 µL or greater. The MultiPROBE® II PLUS HT EX Forensic Workstations are unable to pipette from dead volumes of less than 20 µL, these samples are manually prepared from amplification.

If a re-run rework test is requested (XRRC, XRRC2, RRCW and RRCW2), the amplification batch and sample position must be specified in the Processing comments (Refer to Table 2 above for the corresponding test results). The information is obtained from the Audit Trail (if the sample has been previously amplified multiple times, be careful to choose the correct batch). The information entered needs to be checked by a second case managing scientist and a specimen note entered indicating that the information is correct.

When ordering these reworks the user is prompted to add a processing comment, Enter this information when prompted or it can be added later on the secondary test panels 9PLEX2, XPLEX 2, XPLEX 3, Microcon Casework, NucleoSpin Casework pages in the re-processing comments field.

Amplification products are not kept indefinitely. The availability of a PCR product should be checked prior to ordering a re-run. For more recent batches, the Analytical Section enters audit notes against the amplification batch when the PCR product has been discarded.

If the rework is for a GMIDX re-read, the original Genotyper ID and folder number must be specified in the processing comments. Enter this information when prompted after you enter in the rework code or it can be added on the 9PLEX(2) page in the Microcon processing comment field.

Extra barcodes required for processing of a sample

There is a limit to the number of test codes available for reworks on a single barcode. For 9PLEX or XPLEX case work samples

Extra barcodes are required when:

1. A sample requires further reworking but the available test codes have been used.
2. Re-extracting from a spin basket; this requires an additional barcode as there can only ever be one extract in existence for each barcode.
3. Between 29 October 2007 (when the first automated DNA IQ casework batch was created) and 19 March 2008 (when routine Off Deck Lysis procedures began) the extraction process required some samples to be sub-sampled in Analytical prior to extraction. If this was the case for a particular sample, a specimen note will indicate that the sample was too large and was sub-sampled by Analytical scientists. If satisfactory results were not obtained from the extraction of the portion sub-sampled by Analytical scientists, the remainder of the sample can be requested to be processed under another barcode.
4. Pooling of DNA extracts. Refer to procedure below and QIS 17142 *Examination of Items* for pooling post-batch functionality samples.
5. Dilution of high quantity DNA extracts or inhibitors -Samples that require a dilution greater than 1 in 20 (for 9PLEX) or 1 in 15 (for XPLEX) or have exhausted the available re-amplification test codes will also require an additional barcode to be requested.

If a sample has been completed in DNAMaster/DAD and subsequent reworks are required they are requested in AUSLAB.

To request a connected barcode and connected barcode reworks:

1. View the XPLEX,9PLEX, 9PLEXX or FBOLD page of the sample
2. Press [**SF10**] ***Registration***
3. Press [**SF5**] ***Copy Entry***
4. Scan in the new barcode
5. Change the ***Received*** date to the current date and time
6. Change the ***Collected*** date to the current date and time
7. Change the ***Specimen***
    i. to '***Trans***' specimen type
    ii. to '***Pooled***' specimen type if pooling pre batch samples
    iii. to '***DNAD***' specimen type for diluting samples.
8. Enter the appropriate DNA priority for the sample
9. Enter details in the ***Sample Info 1*** field
    i. If the sample is being transferred from a **XPLEX** or **9PLEX** sample add the source barcode to the ***Sample Info 1*** field.
    ii. If the sample is a pre batch functionality sample then the ***Sample Info 1*** field must contain the DNA# of the sample.
10. Request a 9PLEX or XPLEX test code depending on the request from QPS.
    i. If pooling samples - When prompted to enter a processing comment identify the type of rework required, e.g. Microcon to full
    ii. If diluting, specify the dilution required e.g. 1:100
11. Press [**F4**] Save to complete and save the registration
12. If XPLEX is requested on a pre batch functionality sample, add to the DNA number to the DNAN (**DNA#**) field.
13. If 9PLEX is requested on a pre batch functionality sample, the DNA# must then be entered into the '***Connected barcode***' field.
14. Fill out the connected barcode field (BARCON for 9PLEX), Comment field for XPLEX with the source barcode and from the source barcode identify the connected barcode in the same fields.
15. For pooled samples, Request a **POOLED** test code for each barcode being pooled.
    i. In the 'This lab number has been pooled with Lab Number' field put in the other samples that the sample has been pooled with (**including** the barcode and **DNA#**).
    ii. In the 'Processed Using Lab Number' field enter the extra barcode given for the processing of the pooled samples.
    iii. The 'Reported Under Lab Number' field will be filled in when final results are available

6.4 Manage samples

Sample management refers to the management of an individual sample. It incorporates the necessary steps to be completed in AUSLAB and if a paper case file exists, the information required to be transcribed onto the case file records.

Cases are not usually allocated to an individual case manager/reporter. The exception to this rule may be some urgent or Blue cases, QPS operations, linked cases or sensitive matters. Samples are case managed by staff from the case management lists. However, if at the time of statement allocation there are outstanding results, a reporter can choose to rework or case manage the outstanding results themselves.

Cases with paper files require the epg to be annotated with the results and interpretations. As a minimum, the type of DNA profile. e.g. single source matching UKM1 is required. These annotations need to be signed and dated by the case manager. The historical 'Reported profile' annotation is not required for PP21 DNA profiles. If a re-run (re-CE/ReGS) has been performed the identification of which run used in STRmix is necessary.

6.4.1 Interpret

6.4.1.1 Paired Kinship/Paternity Trios

Any samples for Paternity trios etc. are interpreted as detailed in QIS 25303 *Statistical Analysis for Paired Kinship and Paternity Trio / Missing Child Scenarios*.

6.4.1.2 PP21 interpretation

Statistics for PP21 results are generated by the STRmix™ program as outlined in QIS 31523 *Use of STRmix™ Software*.

If a sample has replicate amplifications they must all be included in the STRmix™ deconvolution unless they have a particular processing issue such as different amplification volumes (half volume vs full volume PCR amplifications), excess peak heights and pull up, a Re-run has been performed or the runs are not consistent with each other (at the discretion of the case manager). A Re-run and the source amplification results cannot be included in the same deconvolution as they come from the same amplification, a choice as to the best or most appropriate run must be made by the case manager, and replaces the less informative result. At minimum, a specimen note (for paperless cases) and an annotation on epg (for paper casefiles) must be added to explain why particular amplifications were not included.

In the instance that a case has had half volume PCR amplifications performed, it is not necessary to include these in the case file as they won't be reported.

All reference samples received for a particular case are to be compared against all interpretable mixtures (to generate a Likelihood Ratio - LR) and single source samples within a case.

The number of contributors will have been determined as per section 6.3.1 above.

Samples processed with STRmix™ V2.0.6 use three populations (Australian Caucasian, Aboriginal and Asian) for the calculation of LRs, the figure that is quoted is the most conservative of the three with a factor of N and 99% one tailed HPD. The case manager is to ensure that this is the figure that is used to determine which EXH line will be used.

Table { SEQ Table * ARABIC } – Quick reference when to use STRmix™

Scenario	Decon	LR
SS <32 & matches assumed known contributor	No	No
SS <32 & matches a reference sample	Yes	Yes
SS <32 & new Unk & NCIDD	Yes	N/A
SS <32 & matches an Unk	No	N/A
First SS >32 DNA profile & matches a reference sample & NCIDD	Yes	No
First SS >32 DNA profile & matches a reference sample no NCIDD	No	No
SS >32 DNA profile & new Unk & NCIDD	Yes	No
Subsequent SS >32 DNA profile and matches a reference sample/Unk	No	No
2P or 3P & no reference samples & not likely to resolve for NCIDD	No	N/A
2P or 3P cond & no other reference samples & not likely to resolve for NCIDD	No	N/A
2P or 3P & reference samples	Yes	Yes

Single source DNA profiles

Deconvolution with STRmix™ is required:

1. If the sample is the first single source DNA profile that matches a reference sample and needs to be loaded to NCIDD or
2. The sample requires loading to NCIDD (e.g. UNK). And/or
3. This DNA profile has a less than 32 alleles.

LR generation with STRmix™ is not required for single source DNA profiles:

1. If a reference sample does not match the single source sample.
2. If a matching reference sample has previously had an LR generated (and the new interpretation would not be more probative).
3. If the single source DNA profile has 32 or more alleles, the sample can be reported with the appropriate EXH line (As per QIS 23008) and doesn't require deconvolution and an LR generated as per the recommendations in the document 'The determination of the threshold number of alleles, above which single source DNA profiles can confidently be ascribed a likelihood ratio in excess of 100 billion.' [Parry et al 2014].

If a single source DNA profile has one peak at a locus and another peak is visible sub threshold, STRmix™ may designate the locus as a homozygote (with a ≥99 % weighting), the case manager should order a rework in an attempt to amplify the second peak.

Homozygote alleles for single source samples that will not be loaded to NCIDD do not require editing in AUSLAB. Homozygote alleles designated by STRmix™ need to be updated in AUSLAB as follows.

1. From the XPLEX screen of the sample
2. Press **[SF7]** ***Results History***
3. Select the appropriate/representative test panel
4. Move the cursor to the allele
5. Press **[F2]** to edit the allele
6. When prompted 'Are you sure (y/n) ?' type 'y'
7. Add the second allele in the format x,x
8. Press **[Enter]**
9. Repeat for the other homozygote alleles
10. Press **[F7] Select Preferred**
11. Press **[SF6] Save Preferred Profile**

A mixed DNA profile would be reported as a single source profile with sub-threshold peaks using the appropriate EXH line (as per QIS 23008) in the following circumstances:

1. If the only indication of a mixture is a labelled Y peak at Amelogenin or
2. If the only indication of a mixture is a labelled Y peak at Amelogenin and sub-thresholdpeaks that do not affect the called alleles.

This is done because STRmix cannot 'see' Amelogenin or sub-threshold peaks and the low level contribution does not affect the interpretation of the 'single source' profile.

Two and three person mixtures

Deconvolution with STRmix™ is not required:

1. If the case does not have any reference samples and the profile is not likely to be deconvoluted by STRmix™ into contributions for NCIDD or

2. If the case does not have any reference samples and if the DNA profile is likely to be deconvoluted into a contribution that matches an already reported unknown in the case. These are reported with the appropriate EXH.

If reference samples are later received they will be compared against the mixture and the LRs reported back via EXH. This is covered in sections 6.5 and 13.1 below.

Deconvolution with STRmix™ is required for all other two and three person mixtures. All three person mixtures have the number of iterations increased to 100 000 burn in and 500 000 accepts.

Two and three person mixtures may run for extended periods of time, additional support is provided by HP2 staff to run deconvolutions on dedicated STRmix™ computers. This releases Reporting Scientists' computers for other tasks.
To have a HP2 staff member run a deconvolution:

1. Add the STRmix™ parameters required as per Table 7 below to the XPLEX comments field.
2. Add your name to the Case Scientist (**XPCM**) field
3. Change the Sample status (**XPRES**) to 'STRmix decon' – the system will list insert the sample to the 'STRMIX' (STRmix decon) list
4. When the STRmix™ deconvolution (and any required reference sample comparisons) have been completed by the HP2 staff member they will change the Sample Status (**XPRES**) to '*STRmix complete'* and the system will list insert the sample to the STRmix CM list
5. The **STRMIXCM** list is sorted by Case Manager then Request Date (in ascending order)

Table { SEQ Table * ARABIC }- Comment for STRMIX list

Decon Interp	**Decon Instruction Truncated**
STRmix™ v1.05	v1
STRmix™ v2.0.6	v2.6
1 contributor	1p
2 contributors	2p
3 contributors	3p
Add c for condition and specify REF name	c SMITH
Add LR for any ref comparisons (add / if after conditioned REF name)	LR (eg. c SMITH/LR)
Decon all runs	No comment added
Decon specific runs	List runs by testcode only eg. XPLEX XAMP1 MCONC1

Conditioning mixtures
It may be possible to condition mixtures from intimate swabs and items (said to have come from a person). The decision to condition is at the discretion of the case manager (and reviewer). Additional information regarding ownership may be required – as per section 6.2.4 above.

Other mixtures
Mixtures that have been assessed as having four or more contributors are considered unsuitable and are not interpreted with STRmix™.

STRmix™ results output

After the STRmix™ deconvolution and/or reference comparison has been completed and processed with the QIS 32139 *STRmix™ Report macro*, the following quality checks must be performed on each result produced by STRmix™.

1. STRmix™ version
2. Casework sample number is correct
3. Reference sample number (if any) is correct
4. Number of contributors assumed to be present is correct
5. Casework DNA profile (correct allelic designations entered and correct run(s) have been included)
6. Individual locus LRs appear have an intuitive fit
7. Check all loci had successfully deconvoluted (component interpretation complete)
8. Settings values (especially check full vs. half variances)
9. Reference DNA profile (correct allelic designations entered)
10. The overall LR is reasonable given the reference and casework DNA profiles

It is important when a STRmix™ analysis is carried out, that the results are interpreted by examining the weightings of various genotypes and the DNA profile(s) observed. There are instances when the results obtained do not intuitively seem correct. Sometimes (particularly if the model must account for drop-in) the failure of the Markov chain to properly converge means that some parameters will not have optimised properly. Examples of this are:

1. Large LRs are obtained for each locus, except one where the LR is low or 0
2. The mixture proportions do not reflect what is observed
3. The degradation does not reflect what is observed
4. Genotype combinations do not reflect all likely allele sets (especially likely if sub-threshold peaks are present at a locus)
5. The probability of dropout at a particular locus has been given a low value but sub-threshold peaks are clearly visible in the DNA profile.

Effectively, a zero LR means that the genotype of the POI has not been accepted by the MCMC at any time through the course of the analysis. Common causes for making a genotype an unlikely contributor are large required dropouts, drop-ins or imbalances, or when the peak heights at a locus exceed the general degradation slope (and are therefore penalised). The standard values for an increased iteration analysis is 100K/500K for burn-in and MCMC respectively. If further iterations are chosen, then the MCMC will have more opportunity to accept the less supported genotypes, however a reference sample with a poor fit to the DNA profile will still have a low LR for a particular locus or loci. It is best practice to attempt to resolve the mixture biologically first, that is through rework, prior to resorting to increased iterations.

If it is noted that the epg has a plate reading error, such as a stutter peak that has been inappropriately removed or an artefact that has been left in, then the sample must be reread and the corrected GMIDX file exported. See section 6.3.4 above.

Paper cases have the STRmix™ report printed and added to the case file, Paper and paperless cases have the results stored on a network drive I:/STRmix results/ .

Repeated Analysis

Each time a DNA profile is analysed using STRmix™ the results will vary slightly. This is a natural consequence of the random nature of the Monte Carlo property. To be as unbiased as possible, each analysis should only ever be run once and the result reported. If a STRmix™ result has been generated for a DNA profile at case management stage, then that same result should be the one used for statement writing. If additional reference

samples are received in the case, the reference sample(s) should be run against all original deconvolutions for all samples in the case where mixtures are present. The exception to this is when an analysis has produced a result that requires further investigation and hence further analysis or if the underlying assumptions made about the profile have changed (eg. a two-person mix is reassessed as being a three-person mix).

Consequently, if at review or at a subsequent stage in reporting it is decided that a different number of contributors better fits the DNA profile, the deconvolution for that sample can be rerun using the new assumption. Case-managers/Reporters should discuss any decision to change a reviewed result with the original reviewer.

If multiple analyses have been conducted, then only the STRmix™ results from the most appropriate analysis should be included in the casefile (e.g. the higher number of acceptances or the more appropriate number of contributors). All relevant STRmix™ results will need to be included in the casefile and previous results removed from the casefile.

The electronic STRmix™ results from the multiple analyses that are not used must be moved into a sub-folder labelled “Do not use” in the case folder in the STRmix results folder.

Use of Ignore Loci function

In certain circumstances a particular locus or loci may be dropped from the interpretation. These include where a Tri-allele pattern has been observed in a reference profile and inconsistent sizing of an allele is observed. There is an option in STRmix™ version 2.0.6 to exclude these loci from the calculations. The Ignore Loci option in the STRmix™ options menu is used. See QIS 31523 Section 8.

Use of the database Search

If there is a large number of reference samples associated to a case, the database (DB) search function in STRmix™ is used. This is the preferred method in this scenario as the number of LR results to be checked and reviewed will be kept at a minimum. The database search function will generate a LR for each reference sample in the file.

Reference DNA profiles that contain partial loci information (e.g. 15, NR) cannot be used in STRmix™ v1.05 or 2.0.6 Database searches. Reference DNA profiles that are partial (whole locus/loci missing) can only be used in STRmix™ v2.0.6 database searches.

A database of reference samples for a particular case is created as per Database search section in QIS 31523.

The created database must be checked by a second case manager/reporter before the database is used in STRmix™. After checking the alleles and sample IDs are correct the checker must replace the case ID on each line with their AUSLAB login mnemonic.

The STRmix DataBase macros incorporates the Factor of N. When the macro is run on STRmix™ V2.0.6 database results, it will ask whether the mixture is 2 or 3 people so that the correct factor can be applied. The reviewer must check that the correct Factor of N has been applied on the printout. It should be 2 for two person mixtures and 6 for three person mixtures.

The results of the DB search are reported back via an EXH (see section 6.5.4). Reference DNA profiles that generate LRs supporting low or non-contributions can be excluded if there are sub-threshold peaks that support the exclusion.

As the DB search does not incorporate the HPD (Highest Posterior Density) or θ (Theta/FST) correction, when a statement is requested, reference samples that give an LR > 0 (except if an exclusion can be made on sub-threshold peaks) need to be compared directly against the original deconvolution to generate an LR incorporating HPD & θ. This ensures that the most appropriate LR is reported in the statement.

Donors of reference samples may be intuitively excluded, in which case the DB search output can be overridden by case managers making this decision (see Appendix 3 – Intuitive Exclusion Guide).

6.4.1.3 P+ interpretation

Samples that are processed with P+ are not interpreted using STRmix™ as this system has not been validated for use with P+ data. Interpretation of P+ samples is outlined in QIS 17168 *Procedure for Single Source DNA Profile Statistics*, QIS 25302 *Interpretation of Mixed DNA (STR) Profiles using Profiler Plus*.

Single source
Single source P+ samples are matched directly against reference profiles and if required for a statement, have a statistic performed as per QIS 17168.

Mixtures
Mixtures are interpreted as detailed in QIS 25302.
P+ mixtures may be transcribed into AUSLAB on the MIXT/MIXC test panels.

Reference samples are compared to the contributions and CODIS Popstats may be used to generate a LR for mixtures that cannot be separated into a major and minor DNA profiles.

Complex mixtures may not have all of the alleles exported from GeneMapper IDx because only 6 alleles per loci are exported and therefore they may not have been identified in the QFLAG checking.

If your profile is able to be interpreted (complex cannot exclude/ complex unable to load, or a major/minor), and at any loci has 7 or more alleles, then an assessment needs to be made to suitability for QFLAG checking. If the major or "large" peaks are captured within the first 6 alleles for each loci, then those peaks have undergone quality flag checking. If any peaks within the major or 'large' peaks fall outside of the first 6 alleles at more than one loci (as the staff match macro allows for 1 mismatch) then a quality flag check can be undertaken for the major/large peaks by the Quality and Projects Senior Scientist. This sample can be inserted onto the BQUAL list with a specimen note "for Quality flag checking". The Quality team or delegate will then perform the quality search on the larger peaks within the profile and add a specimen note, inserting back onto the case managers comms list.

6.4.2 Complete LIMS

AUSLAB is pre-programmed with a number of auto-validation rules to speed up case management. These rules rely on certain conditions being met. At the time that a DNA profile is imported into AUSLAB, auto-validation occurs to allocate the sample to an appropriate hold or case management list. The core comments used by plate readers QIS 31389, direct the sample via test panels that are ordered by the GIDXXPLX or GMIDX auto-validation mask. The system will 'Save prefer' the DNA profile triggering an additional AUSLAB equation to add the completed date and change the sample status to 'Completed' At the end of case management and review of a sample all test panels are required to be fully validated.

For PowerPlex 21 samples (XPLEX request):
Refer to Figure 3 below:
Case managers as a minimum must complete the following fields:

a. XPCM (Case scientist) with their mnemonic
b. XPNR (CM NCIDD) with either "Y" or "N"

Case Managers must also ensure that the

a. XPCD (Completed Date) is populated
b. XPRES (Sample Status) with "For Review"

The essential fields (fields that must be completed for full validation of the request) for XPLEX are:

a. XPCD (Completed Date)
b. XPRES (Sample Status)
c. XPCM (Case scientist)
d. XPNR (CM NCIDD)
e. XPRV (Reviewed By)
f. XPRN (Rev NCIDD)
g. XPDAT (Reviewed Date)

If the Case Manager name and Reviewer name are the same, AUSLAB is programmed to delete the Reviewer.

For COMIX
Case managers as a minimum must complete the following fields:

a. CMXDAT (Date completed)
b. CPROS1 (Profile)
c. CP1N (CM A NCIDD)
d. CPROS2 (Profile) – only if second NCIDD load
e. CP2N (CM B NCIDD)-only if second NCIDD load
f. CMXA01 – CMXA21 (Locus fields)
g. CMIX1-CMIX21 (Allele fields)

The essential fields (fields that must be completed for full validation of the request) for COMIX are:

a. CMXDAT (Date completed)
b. CMREV (Reviewed By)
c. CXMRDT (Reviewed)

For Profiler Plus samples (9PLEX request):
Refer to Figure 4 below:
Case managers as a minimum must complete the following fields:

a. CSCI (Case scientist) with their mnemonic
b. 9PLEXS (DNA Profile Result) with "For Review"

The essential fields (fields that must be completed for full validation of the request) for 9PLEX are:

a. 9PLCD (Completed Date)
b. 9PLEXS (DNA Profile Result)
c. 9PLREV(Reviewed By)

d. 9PLDAT (Reviewed Date)

Mixed DNA profiles that can be interpreted or deconvoluted are displayed in AUSLAB using one of three test panels – MIXT,MIXC (9PLEX samples) or COMIX (XPLEX samples).

For MIXT/MIXC samples:
Refer to Figures 6 & 7 below.
Case managers as a minimum must complete the following fields

a. MIXCD (Completed Date)
b. MIN101 – MIN110 (Known Contributor/Major)
c. MIN201- MIN210 (Remaining Profile/Minor)
d. MIN301-MIN310 (Ratio)

The essential fields (fields that must be completed for full validation of the request) for MIXT/MIXC are:

a. MIXREV (Reviewed By)
b. MIXDAT (Review Date)
c. MIXCD (Completed Date)

Connected barcodes
Once reworks are finalised on a connected barcode, the 'Accepted Barcode' field needs to be filled out. If the original DNAmaster profile is the best profile, enter the DNA# into this field. If the AUSLAB profile is the best profile, add the barcode to this field.

If a NCIDD load is to occur from the original barcode, the DNA profile needs to be manually added to the XPLEX or 9PLEX page. The alleles designations must be checked by the reviewer to ensure transcription errors are avoided

Hold samples
Samples that have been extracted and held (such as epithelial fractions) need to have the XPLEX page completed in AUSLAB. This ensures that laboratory numbers clear outstanding lists and are shown as fully validated in the SF9 summary screen.

1. Enter your name in the XPCM (Case scientist) field
2. Enter 'No' in the XPNR (CM NCIDD) field
3. Enter 'No' in the XPRN (Rev NCIDD) field
4. Enter 'N/A' in the XPRV (Reviewed By) field
5. Validate all test panels for the request

Last sample interpreted in a case
If all of the samples within the case have been interpreted; on the CS test panel change

1. Case status (CASET) to PRSENT – Sent to Peer Review
2. Exhibit (EXRTR) to
    i. Ready to return (no submissions on whole item) or
    ii. Ready to return subsample retained (where one or more submissions from whole items) or
    iii. Destroyed subsample retained (in-tube case)
    iv. N/A (for Paternity cases with FTAs only)

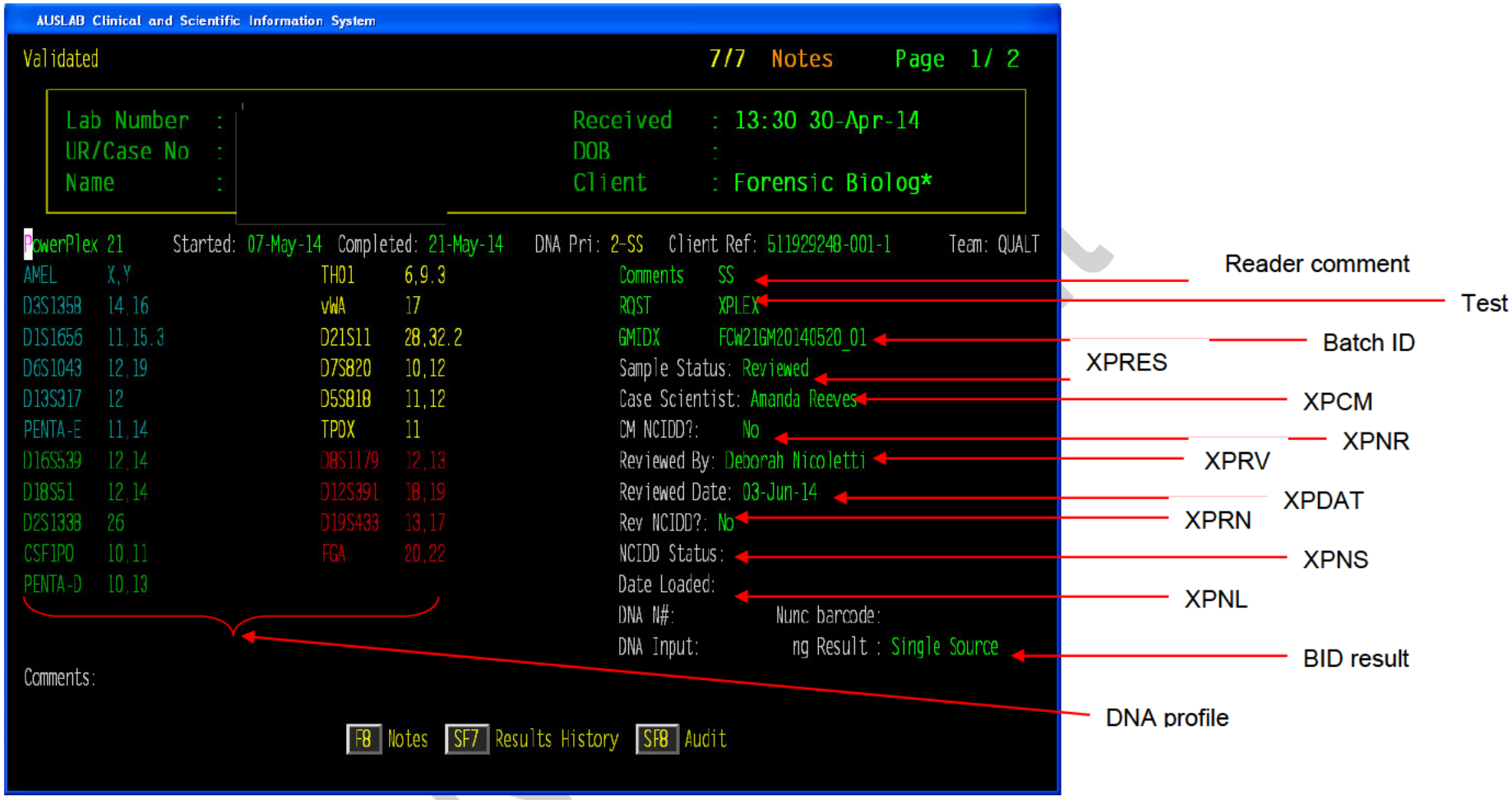

Figure { SEQ Figure * ARABIC } - XPLEX request showing AUSLAB result mnemonics

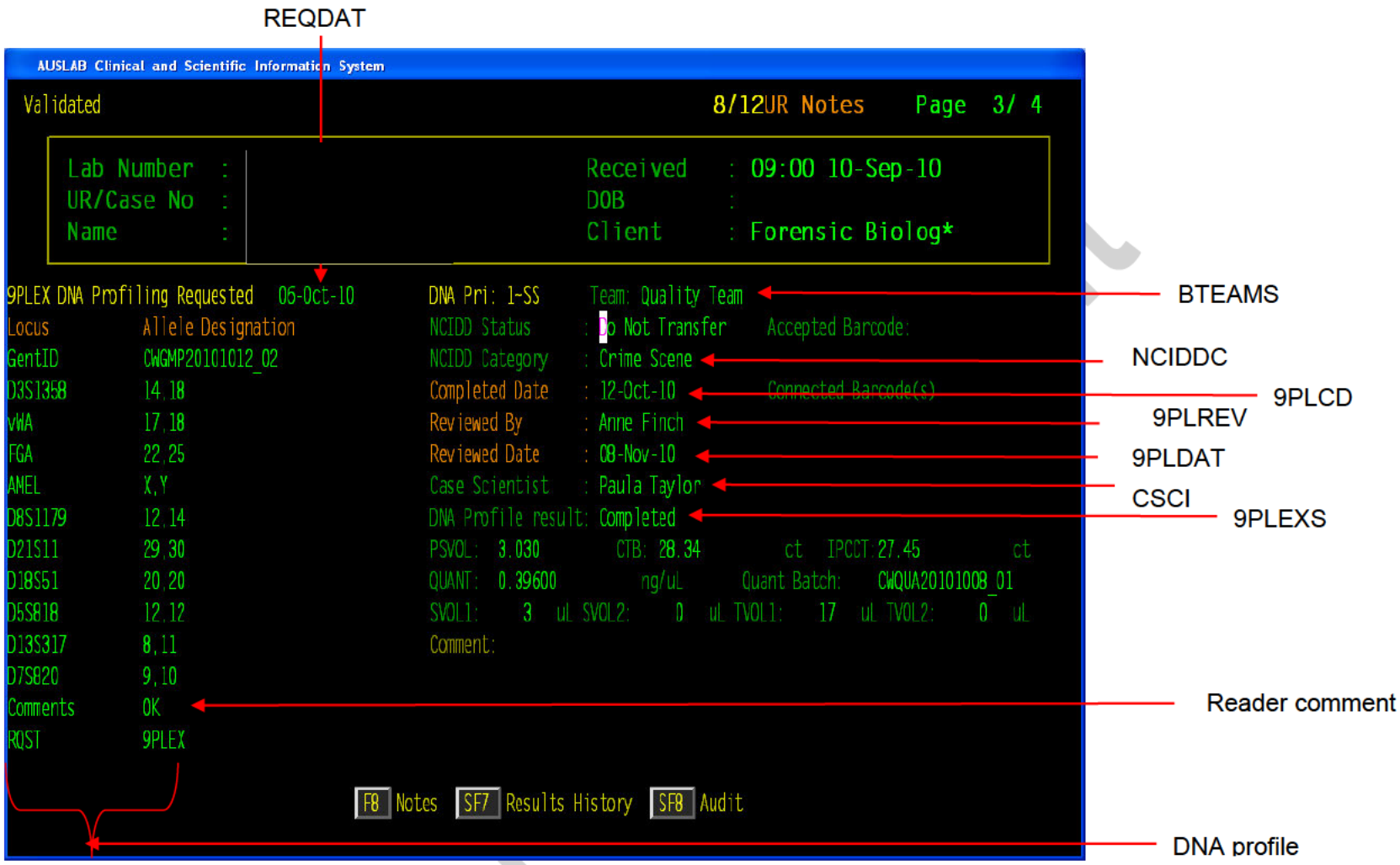

Figure { SEQ Figure * ARABIC } - 9PLEX request showing AUSLAB result mnemonics

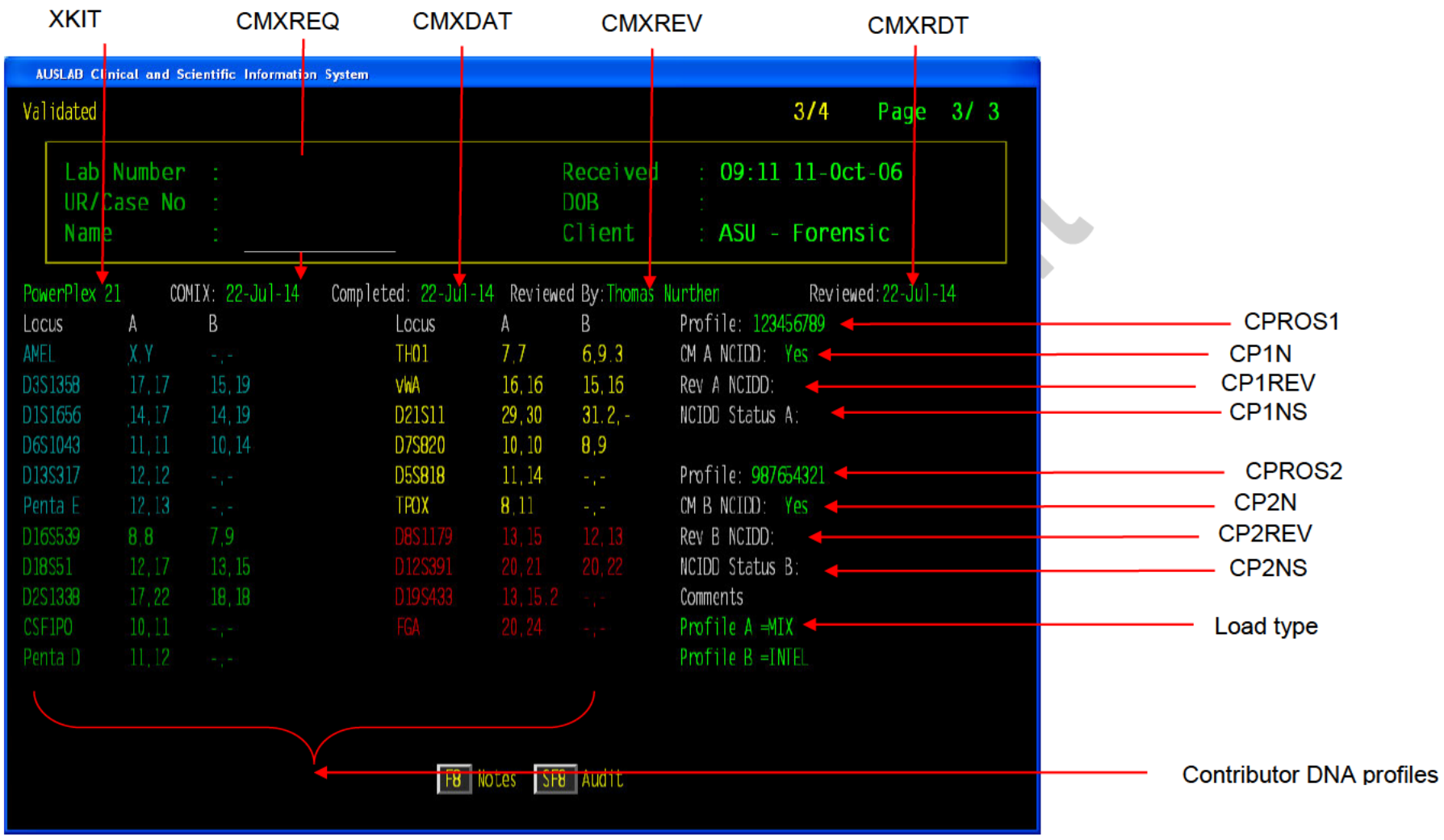

Figure { SEQ Figure * ARABIC } - COMIX request showing AUSLAB result mnemonics

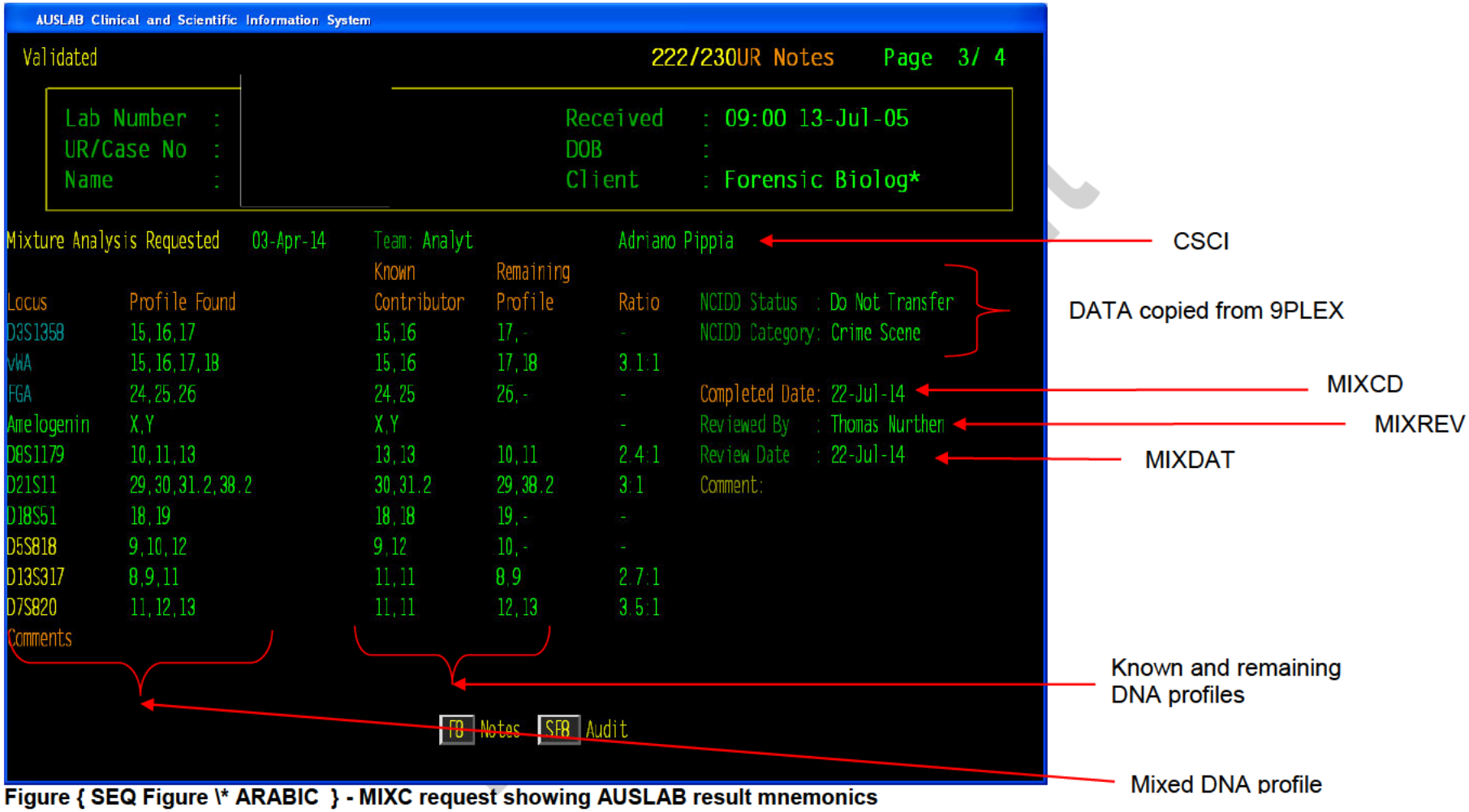

Figure { SEQ Figure * ARABIC } - MIXC request showing AUSLAB result mnemonics

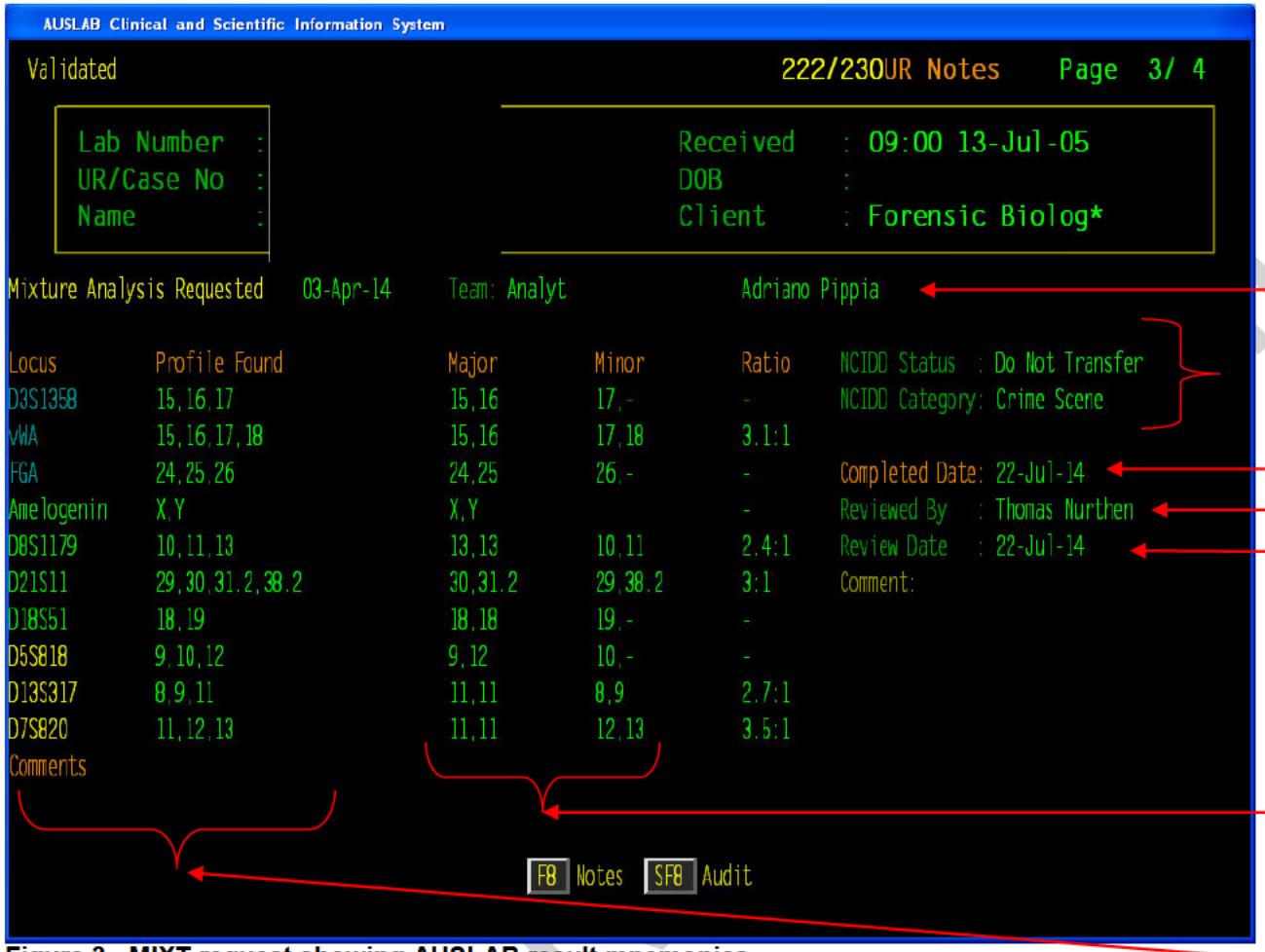

Figure 3 - MIXT request showing AUSLAB result mnemonics

6.5 Report Results

All results are to be communicated as outlined in QIS 23968 *Forensic DNA Analysis Communications Procedure* and QIS 24015 *Procedure for Intelligence Reports and Interstate/Interpol Requests*.
Statements and intelligence reports are to be prepared according to QIS 17119 *Procedure for the Release of Results*.

EXR and EXH pages vary slightly in their appearance however the information entered is the same (for 9PLEX samples). If a case has started processing with EXR lines, additional information must be added to EXR lines NOT EXH lines.

EXH pages for XPLEX samples are the same as for 9PLEX pages, however due to interpretational changes in DNA profiles processed through PP21 most of the EXH lines used will be different. The full list of available EXH lines and the full expansions as seen by QPS is detailed in QIS 23008 *Explanations of EXR/EXH Results*.

NOTE: If a sample cannot be explained by one of the EXH results available, an intelligence letter should be sent to QPS to outline the interpretation. See QIS 24015 .

EXR/EXHs are entered into AUSLAB with the following hierarchy:
If multiple similar results are available for an exhibit with sub samples, the first barcode (e.g. SAIK presumptive has been reported) must always be reported back, if there are subsequent more informative results they are reported from the same EXH

1. Presumptive EXH lines
2. Interim EXH lines (only applicable to DNA Prioritiy1)
3. Final EXH lines
   a. DNA profile type
      i. Complex, Single source,2 person,3 person or Similar
   b. Conditioning information (if applicable)
   c. NCIDD load information (if applicable)
   d. Reference sample comparison interpretations (e.g. STRmix LRs) (if applicable)
4. EXH updates/Incorrects (if applicable)

	Lab No.	Result / Status	Linked No.	Warm Link Name	Peer Review
1	[redacted]	Submitted-results pending.			Rev-Ack 07-Nov-08
2		Interim result- Partial profile undergoing rework			Rev-Ack 17-Jul-14
3		Two person mixed DNA profile			
4		2 person mixed profile - conditioned on	123457666	BURNS	
5		2 person mixed profile - remaining Intel - NCIDD	654321987	SIMPSON	
6		2 person mix profile - support for contrib > 100 billion	654321987	SIMPSON	
7					

Figure 4 - EXH example

6.5.1 Interim EXH lines

Once a rework is ordered, an interim EXH must be entered only for urgent/Priority 1 cases. If the interim EXH that has been selected contains no interpretation, such as 'interim result

– sample undergoing rework', the result can be validated by the person who entered it. If an interpretation is included in the selected interim EXH, such as 'Interim result - Mixed profile obtained - rework reqd', the result must be validated by someone other than the person who entered it (and must be competent to do so).

6.5.2 Final EXH/EXR lines

If the barcode of the final preferred profile is the same as the original barcode used to report the presumptive results, the final result can be reported via EXR/EXH under that barcode.
If the barcode of the final preferred profile is different to the original barcode used to report the presumptive results (but refers to the same sample), an EXR/EXH line explaining why must be entered. The final result is then reported under the barcode that it was processed under.

If a profile obtained from a casework sample does not match any reference profiles within a case (or if the case has no reference profiles) 'UKM1' (for a male profile), 'UKF1' (for a female profile) or 'UKP1' (if gender is undetermined) is entered into the Linked No. field. Each subsequent unknown is given a consecutive denomination, e.g. UKM2, UKM3 etc. This applies to single source samples profiled through PP21. It also applies to single source P+ samples, Major/Minor mixtures and 'Remaining' profiles. See also QIS 31523 .

Example 1 (for 9PLEX/XPLEX samples):
A sample with barcode 111111111 was submitted to Analytical. The sample was diluted in Analytical due to an excessive quantitation value. This diluted sample was assigned the barcode 222222222, and continued through the amplification process. The profile for 222222222 was assessed to be male, full and unique within the case (with no reference profiles). The final EXH below is for a 9PLEX sample –See Figure 9 below. The EXH would be different for a XPLEX sample i.e. 'NCIDD upload single source DNA profile' would be the 'Result/Status' field.

	Lab No.	Result / Status	Linked No.	Warm Link Name	Peer Review
1	[redacted]	Submitted-results pending.			
2		Sample processed and final results under	222222222		
3		9 loci DNA profile. Uploaded to NCIDD	UKM1	[redacted]	

Figure 5 - Example 1 EXH

Example 2 (for 9PLEX/XPLEX samples):
Wet and dry swabs of the handle of a knife were taken and submitted separately to the Analytical section. Exhibit barcode (knife) – 111111111; Wet swab – 222222222; Dry swab – 333333333. The presumptive EXR/EXH was entered under the barcode for the wet swab. Both the wet and dry swabs yielded partial profiles with sub-threshold peaks, and it was decided to pool the samples. Samples were pooled under barcode 444444444 and processed further. A partial profile (13 alleles) matching that of the suspect (John Smith), barcode: 555555555, was obtained. The EXH would be different for a XPLEX sample ie. 'SS DNA profile < 9 loci LR 1 million - 1 billion' would be the 'Result/Status' field. See Figure 10 below.

	Lab No.	Result / Status	Linked No.	Warm Link Name	Peer Review
1	[redacted]	Submitted-results pending.			
2		Sample pooled and processed under	444444444		
3		Partial DNA profile. Uploaded to NCIDD	555555555	SMITH, J.	

Figure { SEQ Figure * ARABIC } - Example 2 EXH

6.5.3 EXH/EXR line updates

EXH/EXR lines may require updating after additional information is available or additional testing has been completed. Commonly, EXH/EXRs are updated after a reference sample for case has been received and new information needs to be sent back to QPS.
If an EXH/EXR has been reported incorrectly (or further information such as ownership becomes available) the line(s) must be incorrected by FRIT Senior Scientists or Team Leader. See Figure 11 below.

	Lab No.	Result / Status	Linked No.	Warm Link Name	Peer Review
1	[redacted]	Submitted for cells. Presumptive saliva test pending.			11-Aug-14
2		Single source DNA profile	UKM1		Incorr. 23-Sep-14
3		Single source DNA profile	UKM1		Reviewed 23-Sep-14

Figure { SEQ Figure * ARABIC } - Example of EXH update

The new correct interpretation is added to the next available line by the case manager and the incorrect line (IRCBx) is changed to 'INR' (Incorrect) by the peer reviewer. The corrected laboratory number must be communicated to QPS DRMU via email (Minor Change register has the most up to date email addresses for DRMU).

If there is a change to the interpretation after the EXH has been reviewed (eg. at statement writing stage), a note in the Specimen notes detailing the reason for the change is a preferable course of action. If there is a significant effect on the result (eg. a NCIDD load and Link are affected and requiring a change), this should be communicated to a Supervising Scientist or Team Leader to inform the QPS DRMU Senior Sergeant prior to sending the email notification.

6.5.4 Suspect checks

If a suspect check has been requested by QPS for a reference sample profiled in P+ and the sample is not intuitively excluded from the mixture, the reference sample needs to be reworked in PP21 to increase the amount of data available to NCIDD and .

Instructions for reworking reference samples are documented in section 9.1 below.

Suspect checks have reserved EXH lines for reporting; refer to QIS 23008 for the appropriate EXH line.

6.5.5 STRmix™ Database searches

For paper based cases – when a STRmix™ DB search is performed, the date of the DB search and the number of reference samples used are included in the Warm link field see Figure 12 below:

	Lab No.	Result / Status	Linked No.	Warm Link Name	Peer Review
1	[redacted]	Submitted-results pending.			Rev-Ack 03-Nov-14
2		Three person mixed DNA profile			
3		Mixture-low support for contrib or supports non contrib		13ref 1uk 4.12	
4		NCIDD upload - mixed DNA profile	UKF2		

Figure 6 - Reporting DB search

If after the LR for the reference samples changes then:

- Add 'This sample has undergone further processing' line
- Add all relevant lines to the interp just like it is being done for the first time. This means, the slate was wiped clean with SUFP so re-add '3MX' etc. etc..
- Do not incorrect any lines
- Do not send an email (DRMU understand the situation may occur)

For paperless cases the date of the DB search and the surnames of the reference samples used are added to a specimen note by the case manager.

6.5.6 Samples with undetermined quantitation values or insufficient DNA

This applies to 9PLEX samples that have an undetermined quantitation value, and for XPLEX samples that have a quantitation value less than the Quantification limit of detection (LOD) which is 0.001 ng/uL.

Competent Analytical Section staff members will case manage these samples. See also QIS *Automated Quantification of Extracted DNA using the Quantifiler Human DNA Quantification Kit* and QIS 24012.

1. Access the **NDNACM** outstanding batches (No DNA Case Management)
2. Create a batch
   a. For 9PLEX samples check that each sample has an IPC <30, the Quant is Undetermined, the Team is Volume & the priority is 3.
   b. For XPLEX samples check that each sample has an IPC <30, the Quant is less than the Quant LOD (0.001 ng/uL)
3. On the 9PLEX/XPLEX page press **[SF7]** ***Results History*** to access the results.
4. Save the profile (which will be blank) by pressing **[F7]** ***Select Preferred*** then **[SF6]** ***Save Preferred Profile***. This will transfer the quantitation information to the 9PLEX/XPLEX page.
5. Add sample management details to AUSLAB
   a. For 9PLEX samples
      a. Add your name to case scientist field - **CSCI** field
      b. Add 'NDNAD' -No DNA detected to the DNA profile result field – **9PLEXS**,
      c. Add today's date to the completed date field on the 9PLEX
      d. On the 9PLEX(2) page, enter the Quant batch ID to complete the batch, and press **[F6]** ***Validate*** the page
6. For XPLEX samples
      a. Add your name to case scientist field - **XPCM** field

b. Add 'N' to **XPNR** field
c. Add 'NDNAD' -No DNA detected to the Sample status field - **XPRES**
d. Add today's date to the completed date – **XPCD** field

7. On the EXH page enter the barcode into the Lab no field of the next blank EXH line and enter 'NDNAD' (no DNA detected) into the result/status field.

   NOTE: if the sample is a sub-sample, the EXH will be entered into the parent barcode (see Client Reference barcode to find parent barcode).
8. Use **[SF9]** to access the results summary page.
9. If the sample is the only sample in the case, or all other samples in the case are also undetermined or completed, then the case can be written off. Enter into the CS test panel and change the case status (CASET) to '*Sent to Peer Review*'

6.5.7 Paternity Samples

For paternity cases, an EXH will have to be registered under a new barcode so that results can be communicated back to QPS via AUSLAB. A follow up phone or email should be made to DRMU to explain the new barcode and EXH. The format for the results to be entered into the new EXH is: child barcode in Lab No. field, profile result in Result/Status field, alleged father/mother in Linked No. field, name in Warm Link Name (of alleged father/mother).

- If a Guthrie card is used and an EXH is registered on that barcode, a subsample barcode will usually be registered for the sample submission. The initial line in the EXH will be: Guthrie card barcode in Lab No. field, profile result in Result/Status field.
- If the putative father sample is an intelligence sample, the relevant EXH would be 'Intel report required for further Interpretation'.
- Consult the Senior Scientist or Team Leader to liaise with DRMU if required to determine the appropriate EXH line to use to best suit their method of reporting.

6.5.8 Using Coronial samples as Reference Samples in EXHs

- If a sample has been processed with casework conditions is to be used as a reference sample, it needs to be deconvoluted in STRmix because there is no homozygote threshold. This deconvoluted DNA profile is used as the reference in all comparisons.
- An EXH is to be requested on the parent barcode of the item (e.g. bone). A subsample for the bone/muscle is to be reported back matching itself, and therefore appear as a reference sample match in AUSLAB.
- This allows the coronial sample to become the reference sample for that continuation of the case.
- Barcode details and person details (Date of Birth, name and type of exhibit) are to be provided to QPS DRMU before the information in the EXH is sent.

7 NCIDD

Case managers are responsible for choosing a representative profile for each unique profile seen within a case for upload to NCIDD. These profiles must have at least 12 alleles for NCIDD matching.

To upload an allele to NCIDD for PP21 samples, a 99% deconvolution is required at a locus as per the Statistics Working Group (STATSWG) recommendations.
e.g.

- [9,11] 99% = 9,11 uploaded
- [9,11] 98% [9,9] 2% = 9,NR uploaded
- [9,11] 98.8% [9,9] 0.6% [11,11] 0.6% = 9,11 uploaded
- [9,11] 98.8% [9,10] 0.6% [10,11] 0.6% = NR,NR uploaded
- If four alleles exist in a deconvolution [9,11] 98.1%[9,10] 0.4% [9,12] 0.5% = 9,NR uploaded
- If in doubt as to the combination to load e.g. [9,10] 98.5% [9,NR] 0.5% [10,NR] 0.5% = NR,NR uploaded
- If in doubt as to the combination to load and the allele count is borderline for NCIDD load (11 alleles) refer to a senior for direction.

≥99% deconvolution at all PP21 loci is known as a 'full' NCIDD load
≥99% deconvolution at ≥ 12 PP21 loci is known as an 'Intel' NCIDD load.

Profiles of less than 12 alleles may be loaded to NCIDD in special circumstances. Please consult with Senior Scientist in the Intelligence Team prior to uploading. All matches generated will be reported through an EXR/EXH. In certain circumstances, a profile with less than 12 alleles (including sub-threshold information) can be loaded to NCIDD, and any matches will be reported back to QPS via an Intelligence report written by the case scientist or Intelligence Team member. This is an intel/upload process and is not for court purposes. Intel/NCIDD work does not get heard in court unless special authorisation is given by the Judge/Justice due to potential to prejudice court.

Only one representative DNA profile is loaded to NCIDD for a person in a case. Profiles that match known deceased persons or complainants in sexual assault cases are not to be uploaded to NCIDD. By the same rationale, unknown DNA profiles previously loaded to NCIDD that match known deceased and sexual assault victims are also removed from NCIDD. Refer to QIS 23890 *Uploading and Actioning Samples on NCIDD* for Forensic DNA Analysis procedure on which case work samples can be uploaded to NCIDD.

7.1 Single Source NCIDD load

7.1.1 9PLEX samples

The steps are listed below to request a load to NCIDD for a single source 9PLEX sample.
The case manager:

- Add the appropriate EXH line as per QIS 23008
- List insert to **NCIDD worklist**

The Intelligence Team:

- Monitor the NCIDD work list
- Request the SNCIDD test panel
- Add 'Load' to the **9PLEXP** field

7.1.2 XPLEX samples

The steps are listed below to request a load to NCIDD for a single source XPLEX sample.
The case manager:

- Adds their name to the **XPCM** field
- Adds 'Y' to **XPNR** field
- Add the appropriate EXH line as per QIS 23008

The Reviewer:

- Adds their name to the **XPRV** field
- Adds 'Y' to the **XPRN**

- Review the EXH line

The Modify 8 equation has been programmed to list insert a sample to the NCIDD list:

1. If **XPNR** is 'Yes'
2. If **XPNR** is 'No' and **XPRN** is 'Yes'

If **XPNR** and **XPRN** are both 'Yes" the sample is removed from the NCIDD list and a SNCIDD test ordered by the system.

7.2 Mixed DNA samples NCIDD load

7.2.1 9PLEX samples

If a mixture is present in a profile and it is possible to separate the mixture into major and minor contributors, or if the mixture can be conditioned against a known profile, a mixture page should be registered and completed in AUSLAB.

The MIXT or MIXC panel is used for 9PLEX samples only. Unlike the COMIX panel, both the mixture and the contributions are displayed on the same panel. The mixed DNA profile will copy from the 9PLEX page (If one exists on the same barcode).

- Add the MIXT/MIXC panel
- Manually add the allele designations of the major/known contributor and the minor/remaining profile
- Add the corresponding ratios (or N/A if not applicable)
- The completed date (**MIXCD**) must also be filled out at the time of the interpretation
- To print the mixture interpretation page for inclusion in the case file press **[SF11]**, then **[F7]** and direct to a printer.
- Add an entry to the **Comment** field on mixture page e.g. 'major – intel load'
- List insert to NCIDD worklist
- Review EXH line, 9PLEX and mixture pages, and the sample is on the NCIDD list.
- List insert to the appropriate review list.

Within high priority cases and low priority cases in exceptional circumstances, mixed DNA profiles can be interpreted for Intelligence purposes and uploaded to NCIDD.
The case manager is required to:

- Add the appropriate EXH line as per QIS 23008
- If necessary, write an Intelligence report

The Intelligence Team:

- Monitor the NCIDD work list
- Request the SNCIDD test panel
- Upload the profile to NCIDD with the suffix '-Intel'.

If an Intelligence report is required, the report will be stored within the Intelligence Team area of Block 6 after it is emailed to QPS DRMU.

7.2.2 XPLEX samples

If a mixture is present in a profile which is assessed by the case manager as suitable for STRmix™ deconvolution and subsequent NCIDD upload, a COMIX test panel is required to be completed and reviewed. Up to two contributors from a mixed DNA profile can be recorded in a COMIX page. If there is a third DNA profile that requires an NCIDD load use the QIS 31512 *Manual NCIDD Upload form PowerPlex®21* form. The EXH reviewer will

then deliver the paperwork to the Intelligence team for upload to NCIDD. Following upload, the paperwork will be scanned into AUSLAB.

- Complete the XPLEX page, Add 'N' to **XPNR** field.
- Request a COMIX test panel
- To add the loci names to the COMIX page, see Appendix 2 in QIS 32019 *Procedure for using the Generic Instrument Interface in Forensic DNA Analysis*.
- Manually add the allele designations from the STRmix™ deconvolution consistently using either a '-' or 'NR' for partial loci. e.g. '15,- ' or '15,NR'
- Add the current date to the **CMXDAT** (***Completed Date***) field.
- Add 'Yes' to the **CP1N** (***CM A NCIDD***) field
- In the **Comments** field add the type of NCIDD load e.g. Intel or MIX

NCIDD loads from COMIX are requested on a different barcode to the source. Each NCIDD upload requires a new barcode for NCIDD upload.

- Press **[SF10]** ***Registration***
- If the **Cli. Ref** is empty add the sample barcode (this allows the source barcode and the NCIDD load barcode to sort together)
- Press **[SF5]** ***Copy Entry***
- Scan a new barcode
- Change the **Received Date** to the current time
- Change the **Collected Date** to the current time
- Change the **Specimen** type to 'Misc'
- If the **Cli. Ref** field is empty then add the source barcode
- Add a designation to the **Sample Info 1** field (e.g. UKM1 or if matching reference Surname.
- Add the NIDD1 request
- Press **[F4] Save**
- Add the new barcode to the **CPROS1** field on the source **COMIX** page.
- List insert to **MIXUPREV** list

Conditioned DNA profiles loading to NCIDD

After a mixed DNA profile has been conditioned in STRmix™, the deconvolution will list that each conditioned allele has been deconvoluted to 100%, a conditioned component of a mixed DNA profile can be loaded to NCIDD provided that :

- The upload alleles are able to be visually separated (i.e. major or minor)
- Upload matching alleles in an even mixture where there is a strong representation

Do not upload contributions from low level mixed minors where we may be confident enough to condition but not load to NCIDD.

7.3 Printing an NCIDD upload form from DADI

Samples that are selected for upload cannot be list inserted on the NCIDD work list and an upload form must be printed and delivered to the Intelligence Team.
To obtain an upload form for a sample on DNAmaster/DAD, open DADI and search for the sample. Click on the Print Upload Form button. Refer to QIS 25583 Use of DNA Analysis Database Interface (DADI).

A barcode may be printed from AUSLAB and attached to the form in the appropriate location for these samples to allow for easier scanning into AUSLAB.

7.4 NCIDD removal

There may be times when a DNA profile that has been loaded to NCIDD needs to be removed or updated with a better DNA profile.

To have a DNA profile removed from NCIDD:
The Case manager is required to:

- Add the barcode of the DNA profile to be removed to the next available row (**EXRL1-21**)
- Add the Result 'DNA profile removed from NCIDD' (PRNCID) to corresponding Result/Status field (**DUM1-21**).

The Reviewer is required to:

- Add the 'Review' to corresponding Peer Review field (**IRCB1-21**)

The Modify 8 equation has been programmed to list insert the EXH barcode to the NCIDD removal list.

The Intelligence Team:

- Monitor the NCIDD Removal list
- Remove the DNA profile from NCIDD
- Update the NCIDD status to 'Removed from NCIDD'

8 Send to peer review

All results must be peer reviewed prior to release to the QPS. Peer review can be at a sample level or case level, Technical or Administrative. QIS 17113 *Technical Review* and QIS 17123 *Administrative Review* outline the procedures involved in review within Forensic DNA Analysis.
Different lists/storage locations are used in AUSLAB for the review of different results. Table 8 below is a summary of the AUSLAB review lists and storage locations.

Table { SEQ Table * ARABIC } - Review lists/storage locations used

Type of result	Test panel	AUSLAB review list
Complex	XPLEX, 9PLEX	COMPREV
Single Source NCIDD	XPLEX,9PLEX	SSUPREV
Single Source	XPLEX	SSREV
Single Source	9PLEX	VCREV
Mix NCIDD	XPLEX,9PLEX	MIXUPREV
Mix	XPLEX	MIXREV
Mix	9PLEX	VCMIX
All unallocated paper	XPLEX	MIXACT
All allocated paper	XPLEX,9PLEX	Individual intray locations

Peer review of 'No DNA detected' and 'DNA insufficient for further processing' is performed by a competent Analytical Section staff member.

1. Access the VOLUND list and check the information completed by the case manager is correct.
2. For 9PLEX samples
    i. Enter your name into the Reviewed by (**9PLREV**) field and
    ii. Press **[F6]** ***Validate*** on each page 9PLEX, 9PLEX(2)
3. For XPLEX samples

i. Enter your name in the Reviewed by (**XPRV**) field
ii. Enter 'N' in Reviewer NCIDD? (**XPRN**) field

4. Review the information entered into the EXH page. If correct, enter 'rev' or 'r' into the corresponding peer review field and press **[F6]** ***Validate***

5. Use SF9 to access the results summary page. If the sample is the only sample in the case, or all other samples in the case are also undetermined or completed, then the case can be written off.
6. Enter into the CS page and change the case status (***CASEST***) to 'Analysed Report not Required' (ARNR),
7. In the date completed field the current date (t) and the exhibits field to 'destroyed, subsample retained' (DESTSR)
8. Press **[F6]** ***Validate*** to validate the page
9. Navigate to the administrative review page and enter your name into both Reviewed by fields, today's date in both Date of review fields, 'N/A' in all other fields except for 'Yes' in the All results checked and validated field
10. Press **[F6]** ***Validate*** the page and remove the sample from the VOLUND list

9 Reference sample management

9.1 Reworking evidence reference samples

Detailed reference processing information is presented in QIS 31389.

GMIDX plate reading comments are the trigger for AUSLAB (via the GIDXR21 autovalidation mask) to automatically rework reference samples. All Evidence reference samples are reworked to yield a full PP21 DNA profile (1 x locus with allelic imbalance and/or incomplete Amelogenin is acceptable). Table 9 below summarises the rework tests available for PP21 reference testing and their equivalent P+ historical tests.

If a buccal FTA sample after the first two direct amplification procedures (1x 1.2 mm spots) fails to yield an acceptable DNA profile; the sample is punched (4x 3.2mm spots), extracted and amplified.
Blood FTA samples due to the potential high concentration of DNA are extracted without any direct amplification.

Table 5 - Reference sample reworks

Description	REF21 Panel	PowerPlex 21 Amp conditions	9FTAR Panel	Profiler Plus Amp conditions
Direct re-amp low conc	R21RUN	1x 1.2 mm spot in 12.5 µL @ 27 cycles	FTARUN	3x 1.2 mm spots in 25 µL@ 25 cycles
Direct repeat analysis issue	R21RPT	1x 1.2 mm spot in 12.5 µL @ 26 cycles	FTARPT	2x 1.2 mm spots in 25 µL@ 25 cycles
Direct re-amp high conc	R21OSD	1x 1.2 mm spot in 12.5 µL @ 25 cycles	FTAOSD	1x 1.2 mm spot in 25 µL@ 25 cycles
Extraction	EREF	N/A	EFTA	N/A
Re-Amplification	R21AM1	Normalised DNA extract to 0.5 ng in 12.5 µL @ 30 cycles	AMP1RE	Normalised DNA extract to 1.2 ng in 50 µL @ 28 cycles
Re-Amplification	R21AM2		AMP2RE	
Re-Amplification	R21AM3		AMP3RE	
Re-Quantification	21REQR		REQR	
Microcon procedure	MCONR		MCREF	
Re-Run	21RRRF	N/A	RRREF	N/A
ReRun	21RRF2	N/A		

If the reworked sample still has analysis issues, the plate reader enters the comment EVDRW and list inserts the sample onto the EVDCM worklist. This worklist is monitored by the Senior Scientist of the Intelligence Team on a weekly basis. The aim is to get a full DNA profile from the evidence samples.

- The rework history is assessed to determine if there is a need for a full PP21 profile
  - Evidence samples that have all of the P+ alleles present and are associated to P+ cases only, can be accepted as complete.
  - Evidence samples that have a replicate sample (e.g. coronial samples may be submitted with a FTA cell sample and a blood sample) that already has a full DNA profile can be accepted within the same case.
  - Evidence samples that are not associated to a case or are partial and don't have matching single source crime scene samples or interpretable mixtures, can be accepted. If however, these conditions change, reworking will be required to obtain a full DNA profile.

Reworking strategies:
After an evidence sample has been reworked via direct amplification, the evidence sample will be sub-sampled, the DNA extracted, quantified and amplified at the optimum DNA input where possible. If an evidence sample fails to generate a usable DNA profile after this process or it has not undergone any direct amplification processing (as in the case of blood FTA samples, evidence swabs and reference hair) additional reworks from the DNA extract may be required.
.
It may be necessary for the case manager to order reworks on evidence reference samples if it has not yet been actioned from the EVDCM work list.

- XS samples – Evidence samples (already extracted) that are excess DNA are reworked by decreasing the amount of DNA template added to the PCR. The 'PP21 half volume SV1 calculation' macro (I:\Macros\PP21 half volume SV1 calculation.xls) can be used to re-calculate the template. The sample is reworked with a Re-amplification test code (As per Table 9). Dependant on how excess these samples are may require several reworks to obtain a full DNA profile.
- NSD samples – Samples that consistently yield NSD or low partial profiles and have low quantitation values are generally reported to QPS as Failed to Profile (FTP). FTP samples are actioned by QPS SMU to submit a further evidence sample, if an additional sample cannot be obtained, and a request is made to be reprocessed and costed, a connected barcode can be used to try to obtain a usable DNA profile.
- Extra peaks – Evidence samples that exhibit extra peaks or other analysis issues require consideration of the previous results obtained. This run may be altered or a previous run that has been confirmed may be accepted. DNA profile edits are processed as per section 6.3.4 above.

It is critical that the correct rework test code is ordered for reference samples via the **[SF7]** ***Results History*** screen for the correct test panel and except for FTAR,FTAREF,FTAR and REF21 must not be ordered via the **[SF10]** ***Registration*** screen. Reference sample reworks must not be ordered with case work test codes.

Once a sample has been processed under an EREF (or for historical samples EFTA/EBLD), an extract exists. If the above reworking techniques have not yielded a full profile, a further extraction can be ordered but must be under a new barcode. There can only be one extract in existence for each barcode.

Connected barcodes
To request a connected barcode and Connected barcode reworks:

1. View the FTAR,9FTAR, REF21 or FTAREF page of the sample
2. Press **[SF10]** ***Registration***
3. Press **[SF5]** ***Copy Entry***
4. Scan in the new barcode
5. Change the ***Received*** date to the current date and time
6. Change the ***Collected*** date to the current date and time
7. Enter the appropriate ***DNA priority*** for the sample
8. Enter details in the ***Sample Info 1*** field ,Enter 'From xxxxxxxxx ' where xxxxxxxxx is the source barcode
9. Request a **REF21** and if necessary a **FTAREF** (to re-bill the request if this process has been requested by QPS on FTA intelligence samples).
10. Press **[F4]** ***Save*** to complete and save the registration
11. Enter the details of the connected barcode in the Comments of the source barcode.

Requesting a REF21 will add the barcode to an outstanding batch allocation dictated by the specimen type. If the connected barcode does not require additional direct amplification (e.g. a microcon) a rework testcode must be ordered (via the **[SF7]** ***Results History***) and the REF21 removed from the batch allocation list as per QIS 24469 (Batch Functionality in AUSLAB) .

9.2 Reporting Reference Samples

Reference samples are collected by QPS under the Police Powers and Responsibilities Act 2000. QPS send registration information to Forensic DNA Analysis via the POLARIS GSI interface (from QPRIME). The NCIDD category and specimen type determine if a reference sample will be loaded to NCIDD.

The same interface sends QPS notification of successful/unsuccessful DNA profiling via the QPSGSI request.

Autovalidation rules have been configured in AUSLAB to automatically request the required test panel (FNCIDD) for loading to NCIDD. For the autovalidation rules to be triggered and result in an FNCIDD being requested the following must occur:

- REF21 must be ordered and
- R21RES (Sample Status) = 'FBPOS' and
- R21NS (NCIDD Status) = 'Load'

If a reference sample has been profiled under a connected barcode, the original source barcode must have the DNA profile and result information transcribed from the connected barcode. This will ensure that the reference sample is able to be validated in AUSLAB and send a result back to QPS. A macro (MOD batch file fix) is used by the Intelligence team to replace the connected barcode with the source barcode in the NCIDD upload file.

9.3 Billing reference samples

New reference samples and reference samples that QPS have specifically requested to be reworked (eg. Upgrade a Profiler Plus profile to PowerPlex 21) are able to be billed via the FTAREF request. For billing to be successful the entire laboratory number must have all of the requests validated.
To check if billing will occur check the specimen audit for the entry as in Figure 13 below.

10:16 25-Jul-14	sys	SS	NIDD4	Episode inserted into consolidation queue CFC ZSS000240
10:16 25-Jul-14	sys	SS	FNCIDD	Episode inserted into consolidation queue CFC ZSS000240
10:16 25-Jul-14	sys	SS	REF21	Episode inserted into consolidation queue CFC ZSS000240
10:16 25-Jul-14	sys	SS	QPSGSI	Episode inserted into consolidation queue CFC ZSS000240
10:16 25-Jul-14	sys	SS	FTAREF	Episode inserted into consolidation queue CFC ZSS000240

Figure 7 - Specimen Audit billing consolidation audit

10 Court Appearances

Notices to attend and give evidence should be recorded in AUSLAB refer to Figure 14 below. Any court appearances should be recorded in AUSLAB. A **CCD** code should be requested and the two pages filled out appropriately.

- The **Date** field (***CSD1-3***) refers to the date of the court appearance
- The **Attended by** field (***CSAB1-3***) refers to the scientist that gave evidence at court
- The **Time Box** (***CSTM1-3***) refers to amount of time giving evidence
- The **Time Out** (***CSTM8-11***) refers to the amount of time the scientist was absent from general duties
- The **Court** (***CSCT1 -3***) refers to the type of court (e.g. Supreme)
- The **Location** field (***CSLOC1-3***) refers to the court location
- The **Trial Type** (***CSTTP1-3***) refers to the type of trial (e.g. Trial)
- The **Evidence** by (***CSEV1-3***) refers to the type of evidence given (e.g. In person)
- The second page of the CCD relates to the content of the court evidence.
- Ensure that the pages are validated by pressing **[F6]** ***Validate***

Court Details

Date	Attended By	Time Box	Time Out	Court	Location	Trial Type	Evidence by	Reviewed by	Pass
29-Jul-14	tenf2	00:30	00:30	Supreme	Rockhampton	Committal	Phone		
30-Jul-14	aapf1	01:00	04:00	Supreme	Rockhampton	Trial	In Person		

Figure { SEQ Figure * ARABIC } - CCD request court appearances

11 Case conferences

The CCD request also provides a table for recording details of case conferences, refer to Figure 15 below.

- The **Date** (***CSD4-7***)field refers to the Date of the case conference
- The **Attended by** (***CSAB4-7***) field refers to the scientist (s) and QPS/DPP staff that attended the case conference
- The **Purpose** (***CSPD1-4***) field refers to the purpose of the case conference.
- The **Time Box** (***CSTM4 -7***) refers to how long the case conference went for
- The **Time out** (***CSTM11 -14***) refers to the amount of time the scientist was absent from general duties
- The details of the case conference can be added to the second page of the CCD or scanned into AUSLAB and the appropriate UR notes added.
- Ensure that the pages are validated by pressing **[F6]** ***Validate***

	Date	Attended By	Purpose	Time Box	Time Out
Conference Details	27-Jul-14	aapf1	Discuss SAIK results	01:00	01:00

Figure { SEQ Figure * ARABIC } - CCD request case conference

12 File compilation

12.1 Suggested order of pages (from top to bottom)

1. Case file particulars page
2. Copy of final statement (if written)
3. Most recent printout of UR notes, emails and other communications*
4. DNA results table (if deemed necessary)
5. Reference samples – receipt page then profile
6. QP127 (if available) and receipt page
7. Examination notes:

a. Description of item
b. Diagrams

8. Photos/photocopies/AUSLAB images*
9. Profiles
10. Mixture interpretation sheets (if applicable)
11. Statistical calculations (if applicable)
12. Subsequent QP127 (if available), receipt page and examination notes etc…

* these items are not required to be printed if the case is not going to court

12.2 Page numbering

Only cases that are going to court (Statements of Witness or Evidentiary Certificates) need to be page numbered. Assistance is available from the Administrative Team for page numbering.

1. The Case File Particulars page is always Page 1 (except upon reactivation when the additional Case File Particulars page will be numbered page 1 and the original Case File Particulars page will be renumbered as the next consecutive number in the case file).
2. Case Files are numbered from the back of the case file to the front.
3. Number and initial each page, including the reverse of the page if both sides have been used.
4. Ensure the Case number is recorded on each page.
5. Write the total number of pages on the front of the case file and initial and date as indicated.

For those cases that aren't going to court, the total number of pages simply needs to be counted and noted on the front of the case file, that is, each individual page does not need to be numbered.

12.3 Statement compilation

Refer to QIS 17119 for the correct format for statements or reports issued by Forensic DNA Analysis.

12.4 AUSLAB finalisation

EXR/EXH page – ensure each sample has the appropriate interpretation entered and validated.
9PLEX/XPLEX page – ensure each sample has a saved preferred profile and validated.
FBEXAM – ensure this page is validated. This page will not validate if required fields do not have entries, e.g. Examination Trolley. Enter N/A or refer to the examination notes for details.
CS – change the status to "Sent to Peer" and validate.
Forensic Receipt page – ensure this page is validated
Return Destruction and Report Release Details – Validate these pages.
Tech Review Page (FBTR) – order an FBTR from the registration page if required, fill in and validate.
FBCALC – order an FBCALC (for 9PLEX samples only) from the registration page if Kinship has been used. Complete and validate

12.5 Preparing a case file for peer review

Prior to submitting a case file for final review or prior to a statement being issued, the following is required:

- Ensure that all items/exhibits have been examined or prioritised appropriately.
- Ensure that appropriate reworks have been performed.
- Establish whether further testing needs to be performed
- Ensure that all samples are finalised and a preferred profile saved on the 9PLEX/XPLEX page.
- Enter the final results in to the EXR/EXH.
- Samples that have been reported as 'No DNA detected' or 'DNA insufficient for further processing' need to be documented in the case file. This can be done by either printing the EXH, annotation of the receipt or annotation of the packaging image.
- All profiles have been printed and included in the case file. Each profile should have a brief description of the sample written on it. An interpretation of the profile must also be written on the epg and signed and dated by the person making that interpretation.
- Ensure that appropriate profiles have been selected for upload to NCIDD. Only one example of each profile is to be loaded to the database.
- Ensure that the reference sample receipt is printed for each evidence sample. To print the reference sample receipt page press SF11, then F7 and direct to a printer.
- If there are multiple epgs for a particular reference sample, only the reported profile need be printed and annotated as the final profile.
- Ensure that all evidence samples associated with the case are present in the final table (if one exists).
- STRmix™ printouts for all paper cases.
- For 9PLEX cases: if a statement has been requested, ensure that profiles requiring a genotype frequency have had the statistical calculation performed through the Kinship program and that the results are printed and included in the file.
- For XPLEX cases: if a statement has been requested, ensure that profiles requiring a STRmix™ interpretation have had the statistical calculation performed through the STRmix™ program and that the results are printed and included in the file.
- For 9PLEX cases: ensure that any mixed profiles have been interpreted using the MIXT or MIXC pages in AUSLAB or the determination of genotypes (if required). A copy of the worksheet or a print-out of the page from AUSLAB should be included in the file.

- For XPLEX cases: ensure that any relevant profiles have been interpreted using the STRmix™ program.
- For 9PLEX cases: if applicable, ensure that any non major/minor or conditioned mixtures are interpreted with appropriate 'Popstats' hypotheses and/or calculations.

13 Reactivated cases and case requiring updated interpretations

13.1 Reactivated cases

On occasion, some cases require further work after they have been finalised and reviewed. When a case file is reactivated the case status must be changed to "Reactivated" and the case completed date should be deleted from the CS page.

A UR note should be entered detailing the reason for the re-activation, e.g. Reactivated for further examination of exhibits, or Reactivated for statement purposes. This is helpful for Property Point when deciding whether or not exhibits can be returned to QPS.

An assessment of previously reported and uploaded profiles should be undertaken. In July 2007, it was decided (in conjunction with QPS) that all crime scene profiles (except Known Deceased and complainants in sexual assault cases) would be uploaded. Prior to this any crime scene sample that matched a complainant profile for any case type was not uploaded to NCIDD. Since the introduction of GMIDX software and lower thresholds, it may also be advantageous to rework samples in an attempt to obtain more information from a profile than may have previously been reported as insufficient for interpretation (if time restrictions permit).

A new case file particulars page is required to easily distinguish between the original section of the file that has been reviewed and the newly added pages.

Any additional Administrative and Technical Review needs to be requested on a new barcode.
Technical reviews are only required on cases with a statement / addendum statement.
If the case was processed using P+, any samples on future receipts for that case will also be processed with P+.

1. If there is a statement request for a low priority (priority 3) volume crime case, and one or more samples have been reported as 'No DNA detected' in the EXH, testing does not recommence. This result will be reported in the statement as 'DNA was not detected in this sample during the initial steps of DNA analysis and as a result no further testing was conducted' (wording is at the discretion of the reporting scientist).
2. If there is a statement request for a low priority (priority 3) volume crime case, and particular sample(s) may benefit from a rework such as a Microcon, the sample(s) can be submitted by the reporter.
3. If a volume crime case (low -3 to high-2 or urgent -1, or sample has its priority changed from low (3) to high (2), and the sample has been previously reported as 'No DNA detected' in the EXH, testing does not recommence. The sample will remain as 'No DNA detected'.
4. If there are samples that have been reported as 'No DNA detected', and written communication is received from QPS that testing is to recommence, these samples will be processed but will not be reworked unless the case priority is changed from low to high.
5. If a high priority case has been tested with P+ and all results were undetermined, additional new items received can be tested with PP21.

13.2 Case requiring updated interpretations – EVDREV

Evidence samples are added to the 1EVD list by Operational Officers when received through list insertion from the case CS test panel. When a reference sample is completed it will be case managed from the 1EVD list.

1. Check Case status
   If there is a paper case and
   a. If the case status is START (Started), print the reference sample epgs and and case manage as a paper file.
   b. If the case status is ARNR (Analysed - Report Not Required) or PRSENT (Sent to Peer Review), the subsequent comparison to reference samples can be performed paperlessly. A note should be made in the UR notes.
2. Change **Case status** to '**REA**' (***Reactivated***)
3. The evidence sample(s) should then be compared to all relevant profiles.
4. Update sample management details
   a. Case manager to delete original case manager and reviewer name, add their name as the case manager.
5. Update the EXRs/EXHs/mixture if required.
   a. If the ref comparison has been conducted and there are no changes to any interpretations, a UR note to say 'ref XX compared to case awaiting review' or similar note is required.
6. Manually list insert case or EXH to EVDREV for review. if there is a new upload for NCIDD, list insert the EXH to SSUPREV or MIXUPREV to enable quick review
7. UR note to be added for 9PLEX/XPLEX cases to say 'comparison complete-awaiting review', change status to 'sent to peer', manually delete sample from 1EVD list.

Cases that have been received and processed using P+ will have any new receipts of casework samples profiled using the P+ system.

New evidence samples received for a case which has been profiled using P+ will be profiled using PP21. Only the 9 common loci between kits will be used for comparison purposes. The EXR/EXH lines used for update purposes will need to be selected appropriate to the kit used for initial processing (P+ / PP21). See also 23008 (Explanations of EXR/EXH Results).

Any interstate person samples submitted for analysis by the DNA Management Section (QPS) that have been obtained from people located interstate are to be treated as Evidence samples (as per advice from the QPS).

14 Case file management off site

When case files are required for court appearances they should be tracked in AUSLAB to the reporting scientist's intray and then the Borrow function should be used.

14.1 Borrowing case files

1. Main Menu
2. Select **2. Sample Processing**
3. Select **7. Sample Storage Search**
4. Enter the barcode and press [**Enter**]
5. Press [**F7**] ***Borrow Sample***
6. Enter a comment when prompted "Please enter borrow comment:'
7. Press [**Enter**]

A comment should be recorded when prompted documenting why the case file is to be borrowed. The person taking the file off site is solely responsible for maintaining chain of custody and confidentiality at all times.

If the case file is requested by court officials a photocopy of the file is to be offered. The case file is the original copy and this must be retained by Forensic DNA Analysis.

There are some rare circumstances where an original case file may be required off-site and not be in the custody of a Forensic DNA Analysis staff member (e.g. Freedom of Information Requests). Where this is the case the Team Leader must be notified in advance and the entire case file must be photocopied and kept within Forensic DNA Analysis. UR notes should be completed explaining the circumstances, where the file is going, provide a contact name if possible and the anticipated return date. When the original case file is returned the copy should be destroyed.

14.2 Returning case files

1. Main Menu
2. Select **2. Sample Processing**
3. Select **7. Sample Storage Search**
4. Enter the barcode and press **[Enter]**
5. Press **[F8]** ***Return Sample***
6. Enter a comment when prompted "Please enter return comment:'
7. Press **[Enter]**

15 Records

1. Case file records – the location of paper case files is recorded in AUSLAB.
2. Paperless case examination notes (FBP1 – FBPX) – all but the current folder is stored in Block 3 Reporting.
3. Batch paper records - Filing Storage area (room 6112) or the Exhibit Room (room 6106)
4. DAD-Prior to AUSLAB Batch Functionality, all results obtained were loaded into an Excel spreadsheet known as DNAmaster. In 2008 these results were transferred to the DNA Analysis Database (DAD).
5. AUSLAB
6. Electropherogram pdf/jpeg files for samples:
   - Genotyper profiles are located in J:\User3100\Results Finalised\PRE-LIMS and I:\User3100\AAARESULTS FINALISED\POST-LIMS
   - As of the 16th February 2009, results have been analysed using GeneMapper ID-X. GeneMapper ID-X profiles are located in P:\Profile PDFs and only accessible from computers with GeneMapper ID-X installed (contains all DNA profile results from 16th February 2009 until June 2012).
   - As of July 2012, all DNA profile results are located in O:\Profile PDFs (accessible from all network PCs).
7. STRmix™ result files are stored on a network drive - I:\STRmix Results\

16 Associated Documentation

QIS: 16004 – AUSLAB Users Manual - DNA Analysis

QIS: 17038 – Case File Particulars

QIS: 17113 – Technical Review

QIS: 17116 – Processing DNA Exhibits/Samples in the Forensic Sciences Property Point

QIS: 17119 – Procedure for the Release of Results

QIS: 17123 – Administrative Review

QIS: 17137 – Procedure for STR fragment analysis using GeneMapper ID-X software

QIS: 17142 – Examination of Items

QIS: 17168 – Procedure for Single Source DNA Profile Statistics

QIS: 19544 – Concentration of DNA Extracts using Microcon Centrifugal Filter Devices

QIS: 33407 - Quantification of Extracted DNA using the Quantifiler® Trio DNA Quantification Kit.

QIS: 20967 – NucleoSpin® method for DNA extraction and clean-up of DNA extract

QIS: 23008 – Explanations of EXR/EXH Results

QIS: 23959 – Storage Guidelines for Forensic DNA Analysis

QIS: 23968 – Forensic DNA Analysis Communications Procedure

QIS: 24012 – Miscellaneous Analytical section Tasks

QIS: 24015 – Procedure for Intelligence Reports and Interstate/Interpol Requests

QIS: 24126 – Forensic DNA Analysis Administrative Officer Case Management

QIS: 24469 – Batch Functionality in AUSLAB

QIS: 24486 – Explanations of Analytical test codes and Batch types

QIS: 25302 – Interpretation of Mixed DNA (STR) Profiles using Profiler Plus

QIS: 25303 – Statistical Analysis for Paired Kinship and Paternity Trio / Missing Child Scenarios

QIS: 25368 – Kinship Software – Genotype Frequency Module

QIS: 25583 – Use of the DNA Analysis Database Interface (DADI)

QIS: 25581 – Kinship Software - Paired Kinship and Paternity Trio/Missing Child Modules

QIS: 31389 – STR fragment analysis of PowerPlex® 21 profiles using GeneMapper® ID-X software

QIS: 31512 – Manual NCIDD Upload form PowerPlex 21

QIS: 31523 – Use of STRmix™ Software.

QIS: 32019 – Procedure for using the Generic Instrument Interface in Forensic DNA Analysis

QIS: 32172 – GII filemaker

17 References

National Association of Testing Authorities (NATA). Forensic Science ISO/IEC 17025 Application Document, July 2015. Refer to NATA website: http://www.nata.com.au

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Parry, R., Caunt., E & Allen C., (2012) Verification of the DNA profile module of STRmix™ using the Promega PowerPlex® 21 system.

Parry, R., Caunt., E & Allen C., (2013) Verification of the DNA profile module of STRmix™ for Full Volume Amplifications using the Promega PowerPlex® 21 system.

Parry,R., Howes, J., & Allen, C. (2014) The determination of the threshold number of alleles, above which single source DNA profiles can confidently be ascribed a likelihood ratio in excess of 100 billion.

Police Powers and Responsibilities Act 2000, Current as of 22 September 2014

Police Powers and Responsibilities Regulation 2012, Current as of 22 September 2014

Howes, J., (2010) A guideline for the assessment of complex DNA profiles.
Caunt, E., Morgan, R., Gardam, T.,Howes, J. & Allen, C. (2014) Verification and implementation of STRmix™ V2.0.1.

Morgan, R., & Caunt E. (2015) Assessment of the Number of Contributors for Mixed PowerPlex® 21 DNA Profiles within Forensic DNA Analysis.

Caunt E., Morgan, R., Howes, J & Allen, C. (2015) Assessment of the Number of Contributors for Mixed PowerPlex® 21 DNA Profiles within Forensic DNA Analysis_version 2

18 Amendment History

Revision	Date	Updated By	Amendments
1	11 Nov 1998	V Ientile	
2	28 Mar 2001	V Ientile	
3	11 Jun 2001	V Ientile	
4	18 Jul 2001	V Ientile	
5	08 Jan 2002	V Ientile	9(3) – Completed case codes for FACTS
6	21 Nov 2002	V Ientile	Changes to section 9, completing a case
7	19 Nov 2003	V Ientile L Freney	Refer to AUSLAB. Remove FACTS in many places
8	07 Jun 2005	M Gardam	Included requirements for paperwork in case file ie No loose pages
9	03 Aug 2006	M Gardam	List of reference articles added
10	25 Sep 2006	M Gardam	Off site case file management, compilation of case file, case management.
11	13 Feb	L Weston	Update with processes for AUSLAB

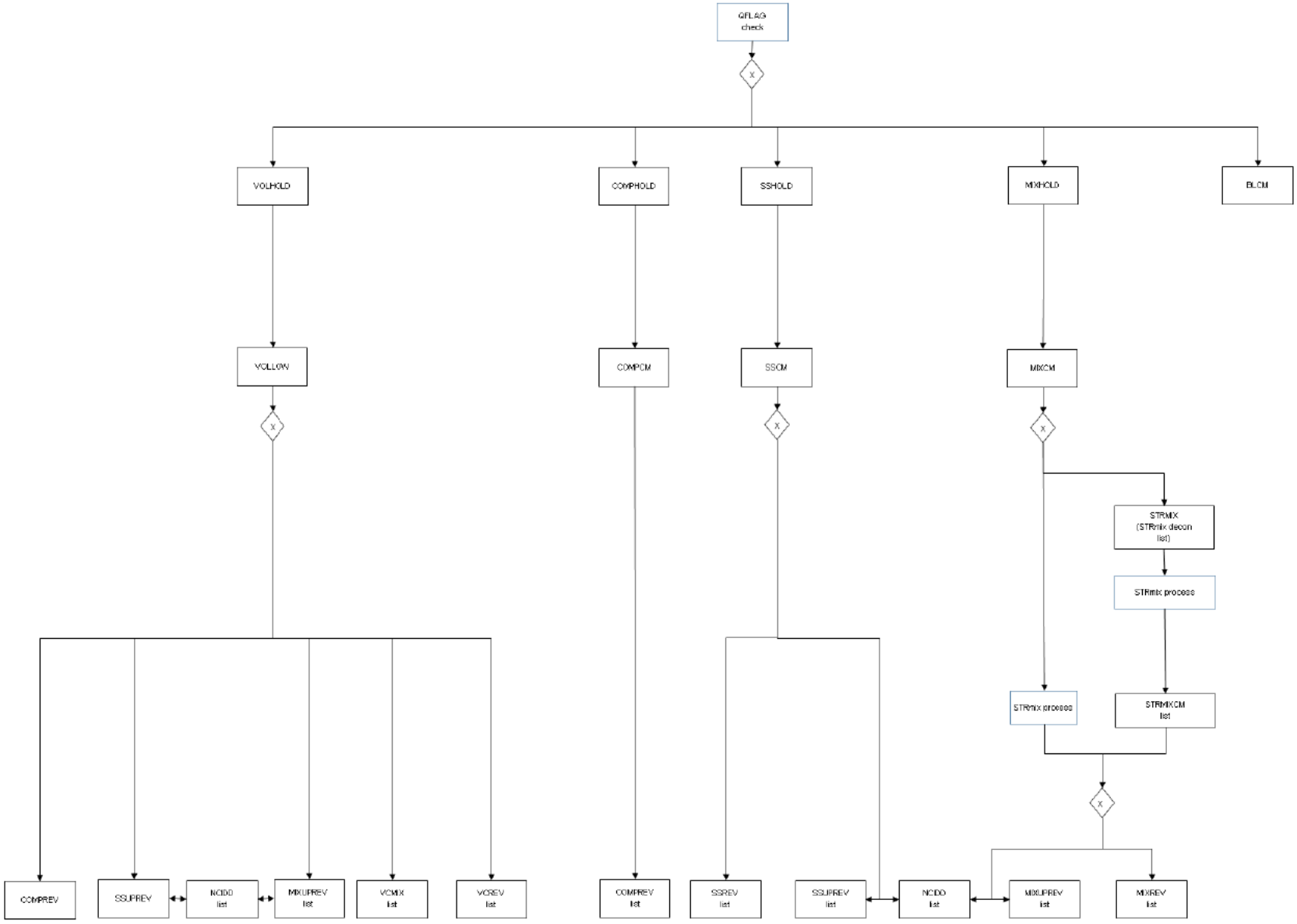
	2007		
12	Apr 2008	QIS2 Migration Project	Headers and Footers changed to new CaSS format. Amended Business references from QHSS to FSS, QHPSS to CaSS and QHPS to Pathology Queensland
Version	**Date**	**Updated by**	**Amendments**
12	10 Apr 2008	J Connell	Transferred section on preparing case file for presumptive EXR/EXH validation to Examination of Items SOP
13	12 Feb 2009	K Lee	Major rewrite; Inserted subheadings and table of contents; changed order of information to reflect current processes; expanded on reworking information and other processes undertaken as part of case management; added information regarding dilutions and requesting processing of samples sub-sampled in analytical; summarised finalisation requirements for samples with extra barcodes; added examples for entering final EXR lines. Hyperlinked associated documents.
14	28 Oct 2009	K Lee	Updated with reference to GeneMapper *ID-X* software; changed "Pre/Post LIMS" references to "Pre/Post AUSLAB Batch Functionality"; removed unnecessary flow charts; updated hyperlinks and associated documents; introduced paperless case management; re-arranged for better flow and grammatical correctness; Introduced more definitions; included instruction on locating profiles for printing.
15	27 Jan 2012	K Pippia	Introduced new worklists; added section on reworking evidence samples; added VOLUND process; addressed changes in processes since last update; removed references to re-Genescanning and introduced references to re-reads; updated hyperlinks; addressed comments raised against last revision; updated FBNLR process
16	12 Nov 2012	Alicia Quartermain, Emma Caunt, Justin Howes	Updated all processes to include implementation of PowerPlex®21 and STRmix™
17	Jan 2015	Thomas Nurthen	Incorporation of updated workflows, major rewrite , New template
18	August	Thomas Nurthen	Fixed typos, referenced new

	2015		document for number of contributors, additional steps for FBNLR process, added NCIDD removal process, updated STRmix versions, NCIDD load requirements
19	07 April 2017	Justin Howes	Changed example on p41 to [9, NR]; added information to 5.4 regarding strmix instructions; added eg P+ to PP21 to 9.3; section 6.3.6 – added info on P+ and microcon instructions; changed LOD Quant from 0.00214ng/uL to 0.001ng/uL; added information to 6.5.3 re incorrects; added first line to Table 6;added information to 6.2.5 on no further work process; added Appendix 3 – Intuitive Exclusion Guide and details to 6.4.1.2; changed 19977 to 33407; fixed title of 24126 and hyperlinking throughout; edited amendment history versions/revisions to align with QIS.

19 Appendices

1 Appendix 1 Case management overview
2 Appendix 2 Case management checklist
3 Appendix 3 Intuitive Exclusion Guide
4 Appendix 4 Quantification workflow

19.1 Case Management overview



19.2 Case Management Check list

Check Quality

- ☐ Batch statuses are fully completed
- ☐ Check specimen notes
- ☐ Check UR notes
- ☐ Check the photo of the crime scene envelope.

Check case

- ☐ Check for Reference samples.
- ☐ Check for Allocation
- ☐ Check for paper file.
- ☐ Ownership of item
- ☐ Case status

Assess results

- ☐ View results already reported
- ☐ Assess the number of contributors to the DNA profile.
- ☐ Assess the quality of the DNA profile
- ☐ Rework DNA extract if necessary/possible
- ☐ Variant/OLA /ULP calculations
- ☐ DNA profile edits

Manage Samples

- ☐ Interpret - STRmix™, POPSTATS etc
- ☐ Reference comparison
- ☐ LIMS completion
- ☐ Paper case files

Report results

- ☐ DNA profile type line
- ☐ Conditioning information line if necessary
- ☐ NCIDD load lines if necessary

Send to peer review

- ☐ List insert to peer review list or track casefile to location

19.3 Intuitive Exclusion Guide

Guide for performing intuitive exclusions

Once the scientist has made an assessment of the number of contributors to a DNA profile, the next stage is to compare DNA profiles obtained from reference samples associated to the case to determine whether these people could be potential contributors. For a single source DNA profile, this is a simple process since the reference sample must match all alleles present within the crime scene profile in order for it to be considered a potential contributor. This process is more complex for mixed DNA profiles as there are more allelic peaks, and combinations of these peaks, to be considered.

As an example, for a two person mixture where there are four alleles at a locus, the reference sample must match two of those alleles to be considered as a potential contributor. If this condition is not met then, under the assumption of two contributors, the reference profile is excluded.

As the number of contributors increase and/or the contributor proportions change, the decision process for excluding a reference profile also changes.

The table below provides a guide for when a reference sample can be excluded as a potential contributor to a DNA profile when comparing the reference sample to an individual locus. It describes the following:

- the mixture type that may be encountered;
- the component of the mixture to which the reference sample is being compared (for an even mixture this would be the entire mixture, for the minor component of a major/minor mixture this would be only the minor alleles);
- the type of match to the reference sample (one or two alleles matching and whether the reference sample is homozygous or heterozygous at that locus).

Where there is an 'S', this means that the reference sample may not be able to be excluded intuitively and that a LR should be calculated using STRmix™. Where there is an 'x', this means that the reference sample can be excluded without the need to calculate a LR in STRmix™.

The number of alleles being compared does not include peaks that could be -2, -1 or +1 repeat stutter. These alleles can be either above or below the LOR but must be above the LOD.

The 'component' of the mixture being compared refers to whether the scientist is comparing to the whole mixture as in an even mixture, or to part of the mixture e.g. major, minor, remaining.

Mixture Type	Number of alleles at locus being examined in component of mixture being compared	Reference sample			
		Doesn't match any alleles	Homozygous matching 1 allele	Heterozygous matches 1 allele	Matches 2 alleles
2 person even mixture - drop-out is unlikely to have occurred	1	x	S	x	n/a
	2	x	S	x	S
	3	x	S	x	S

	4	x	x	x	S
2 person even mixture - drop-out is <u>likely</u> to have occurred	1	S	S	S	n/a
	2	S	S	S	S
	3	x	S	S	S
	4	x	x	x	S
2 person major/minor mixture **- comparison to minor** (major is considered single source)	1	x	S	S	n/a
	2	x	x	x	S
2 person conditioned mixture **- comparison to remaining**	1	x	S	S	n/a
	2	x	x	x	S
3 person even mixture - drop-out is <u>unlikely</u> to have occurred	1	x	S	x	n/a
	2	x	S	x	S
	3	x	S	x	S
	4	x	x	x	S
	5	x	x	x	S
	6	x	x	x	S
3 person even mixture - drop-out is <u>likely</u> to have occurred	1	S	S	S	n/a
	2	S	S	S	S
	3	S	S	S	S
	4	S	S	S	S
	5	x	S	S	S
	6	x	x	x	S
3 person major/minor mixture - 2 people in major - drop-out of major is unlikely to have occurred **- comparison to major**	1	x	S	x	n/a
	2	x	S	x	S
	3	x	S	x	S
	4	x	x	x	S
3 person major/minor mixture - 2 people in major **- comparison to minor** (minor single source)	1	x	S	S	n/a
	2	x	x	x	S
3 person major/minor mixture - 2 people in minor **- comparison to minor** (major is considered single source)	1	S	S	S	n/a
	2	S	S	S	S
	3	x	S	S	S
	4	x	x	x	S
3 person conditioned mixture - 2 people in remaining **- comparison to remaining**	1	S	S	S	n/a
	2	S	S	S	S
	3	x	S	S	S
	4	x	x	x	S
3 person conditioned mixture - remaining is 2 person major/minor **- comparison to remaining minor** (single source) (major is considered single source)	1	x	S	S	n/a
	2	x	x	x	S

19.4 Quantification workflow